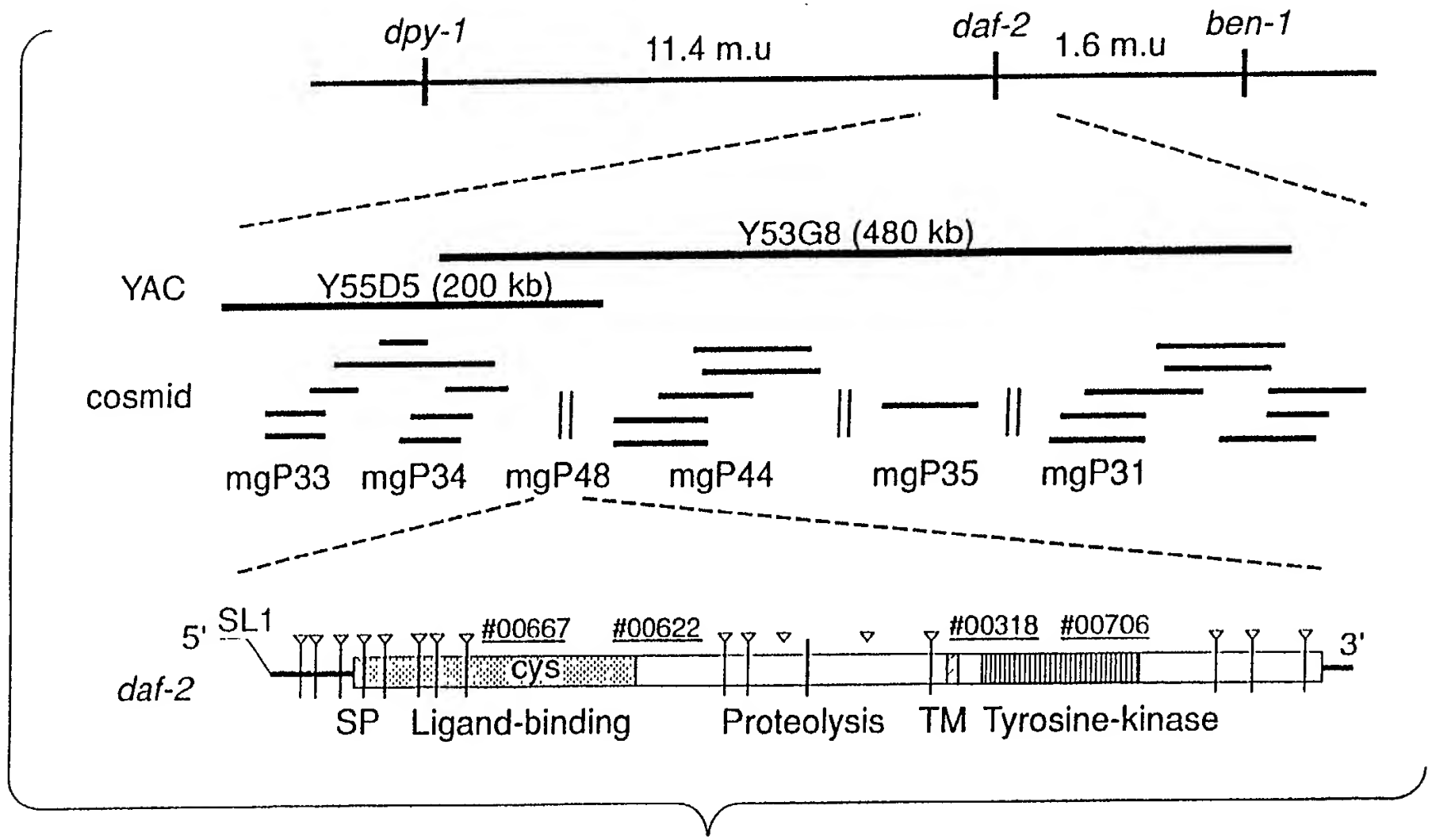
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SL1
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cys
3'
daf-2
SP
Ligand-binding
Proteolysis
TM
Tyrosine-kinase

Fig. 1

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 541 VFFSWPSFNITDIDQRKFLGYELFFKEVPRIDENMTIEEDRSACVDSWQSVFKQYYETSN
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```

Fig. 2A

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Fig. 2B (sheet 1 of 3)

```
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Fig. 2B (sheet 2 of 3)

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Fig. 2B (sheet 3 of 3)

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  DInR RGGVRIEKNHKLCYDRTIDWLEILAENESQLVVLTENGKEKECSLSKCPGEIRIEEGHDNTAIEGELNASCQLHNNRRLCWNSKLCQTKC......PEKC
 DAF-2 NGGVRIIDNRKLCYTKTIDWKHLITSSINDVVVDNAAEYAVTETGLMCPRGACEEDKGESKCHYLEEKNQEQGVERVQSCWSNTTCQKSCAYDRLLPTKE

                      R                                                P
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                                                                                                  L(mg43)
                          Y(mg43)                                                                 vS(sa187)
                                                                                        R
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   InR SSN.LLCTPCLGPCPKVCHLLEGEKTIDSVTSAQELRGCTVINGS..LIINIRG..GNNLAAELEANLGLIEEISGYLKIRRSYALVSLSFFRKLRLIRG
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                                                                                E S
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  DInR DPPMDADKYALYVLDNRDLDELWG.PNQTVFIRKGGVFFHFNPKLCVSTINQLLPMLASKPKFFEKSDEGADSNGNRGSCGTAVLNVTLQSVGANSASLN
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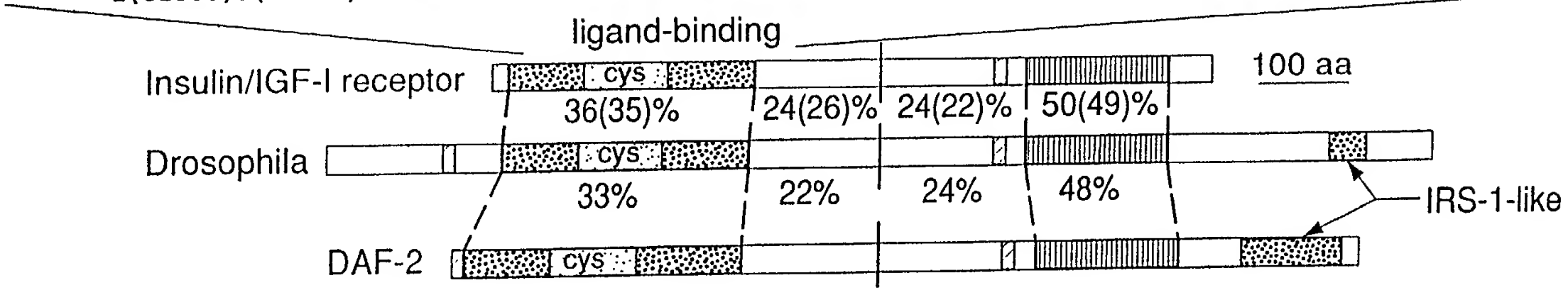


Fig. 2C (sheet 1 of 2)

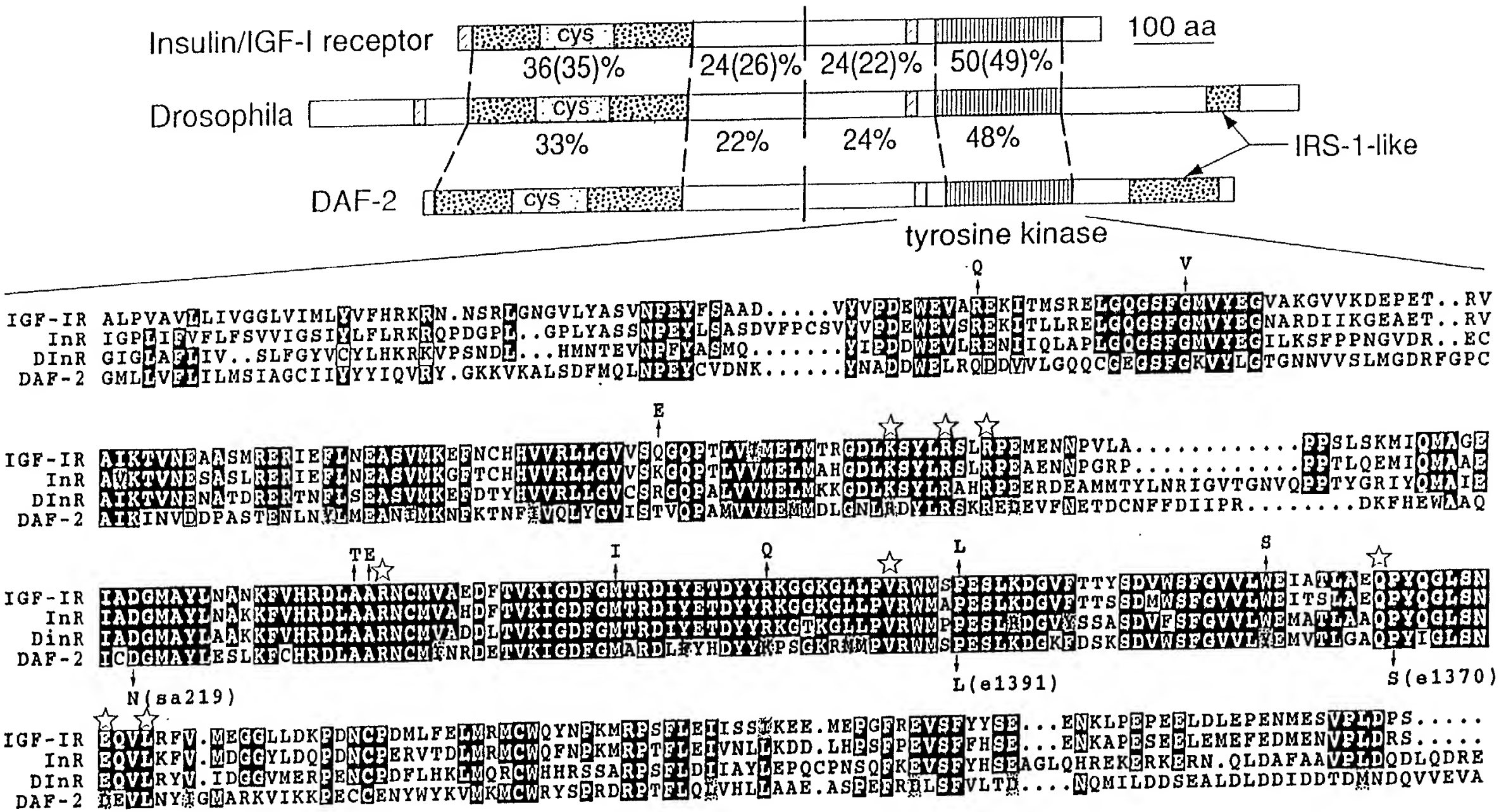


Fig. 2C (sheet 2 of 2)

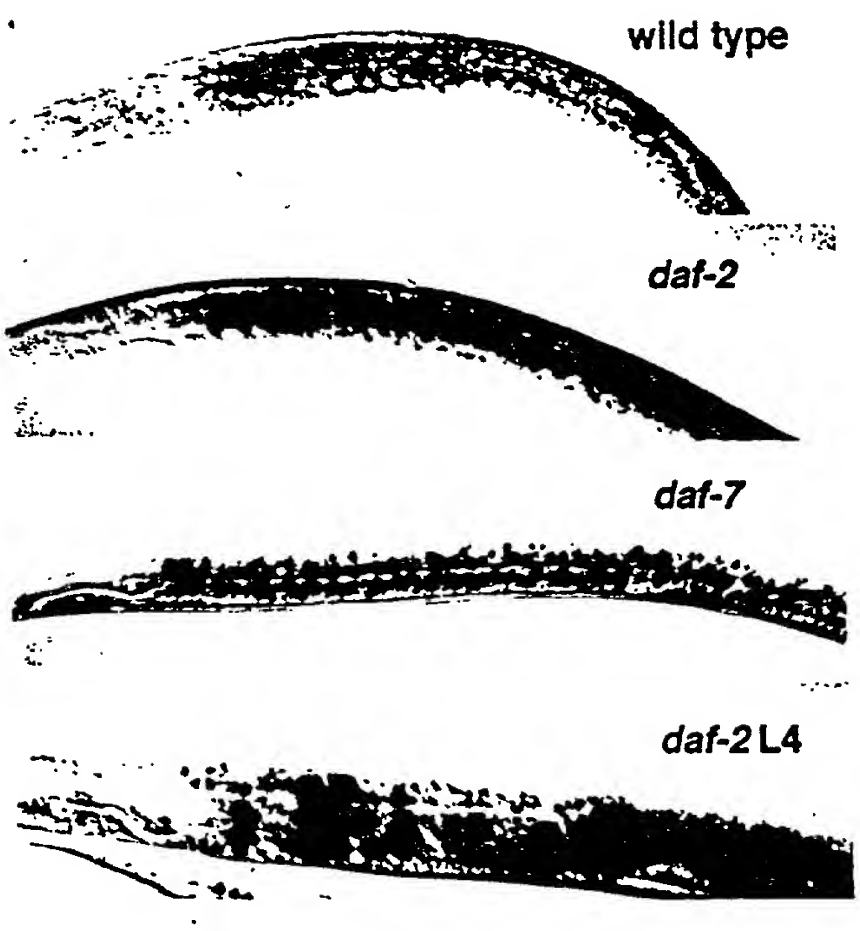
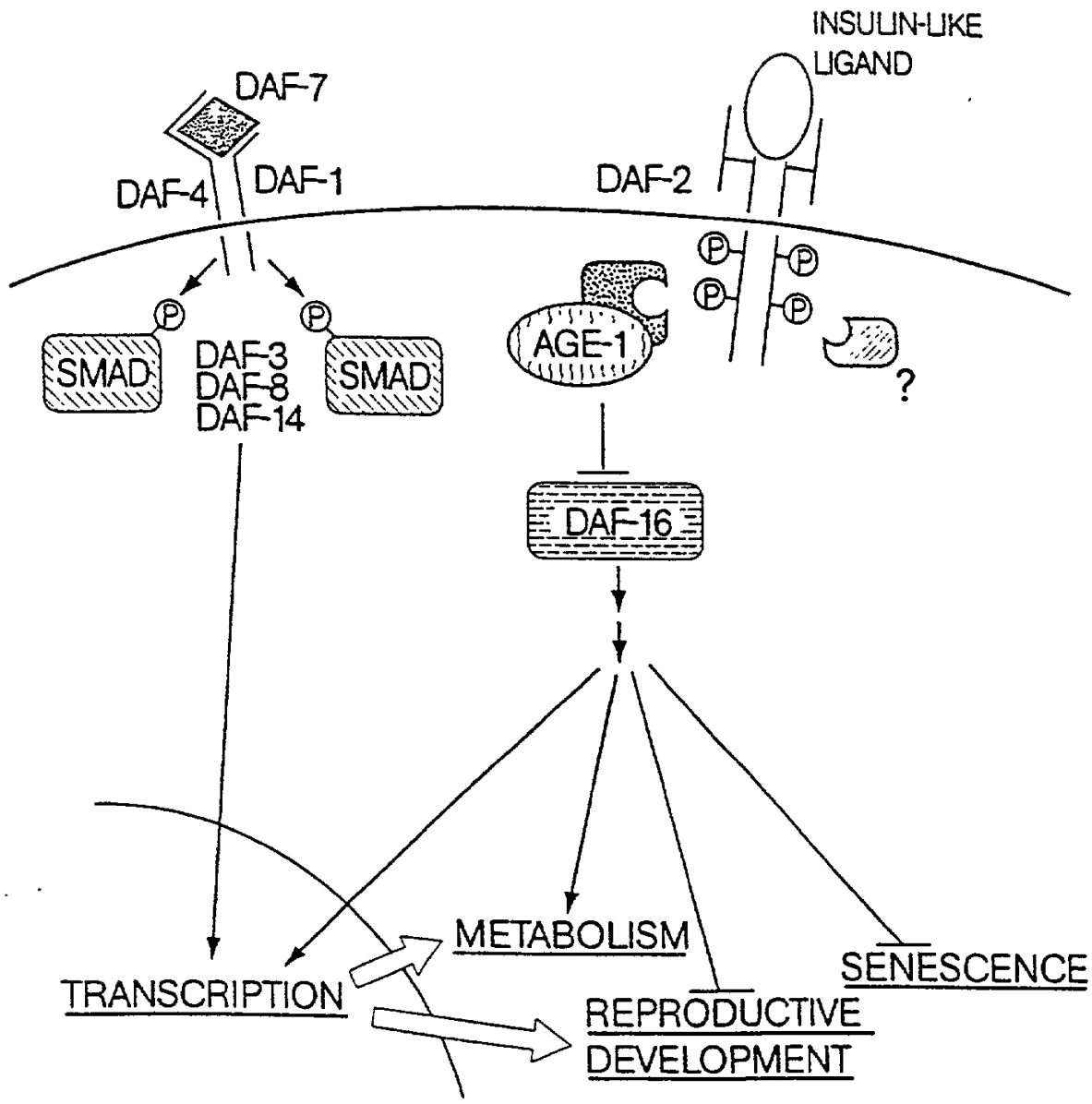


Fig. 3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LIGAND
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DAF-4
DAF-1
DAF-2
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SMAD
DAF-3
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?
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METABOLISM
SENESCENCE
TRANSCRIPTION
REPRODUCTIVE
DEVELOPMENT

Fig. 4

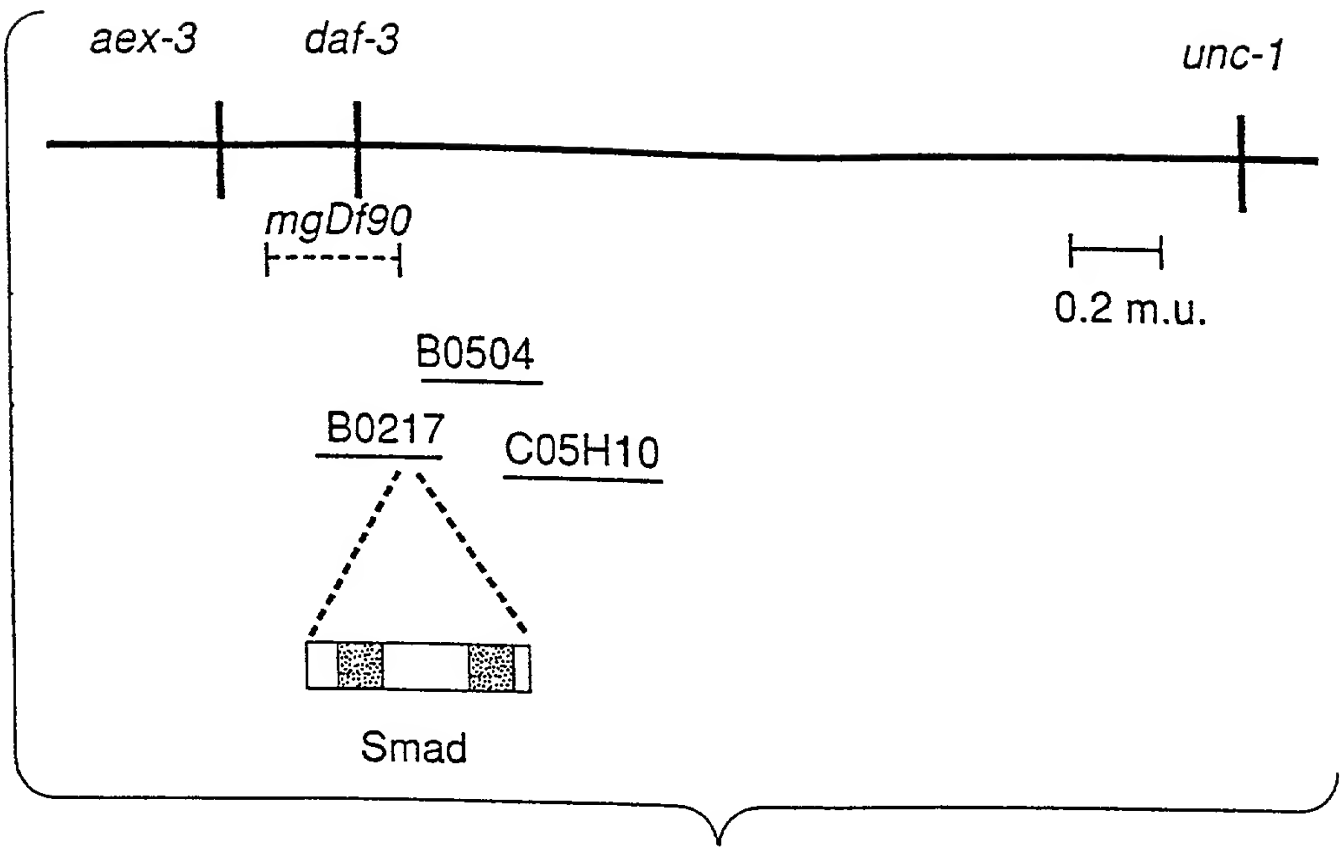
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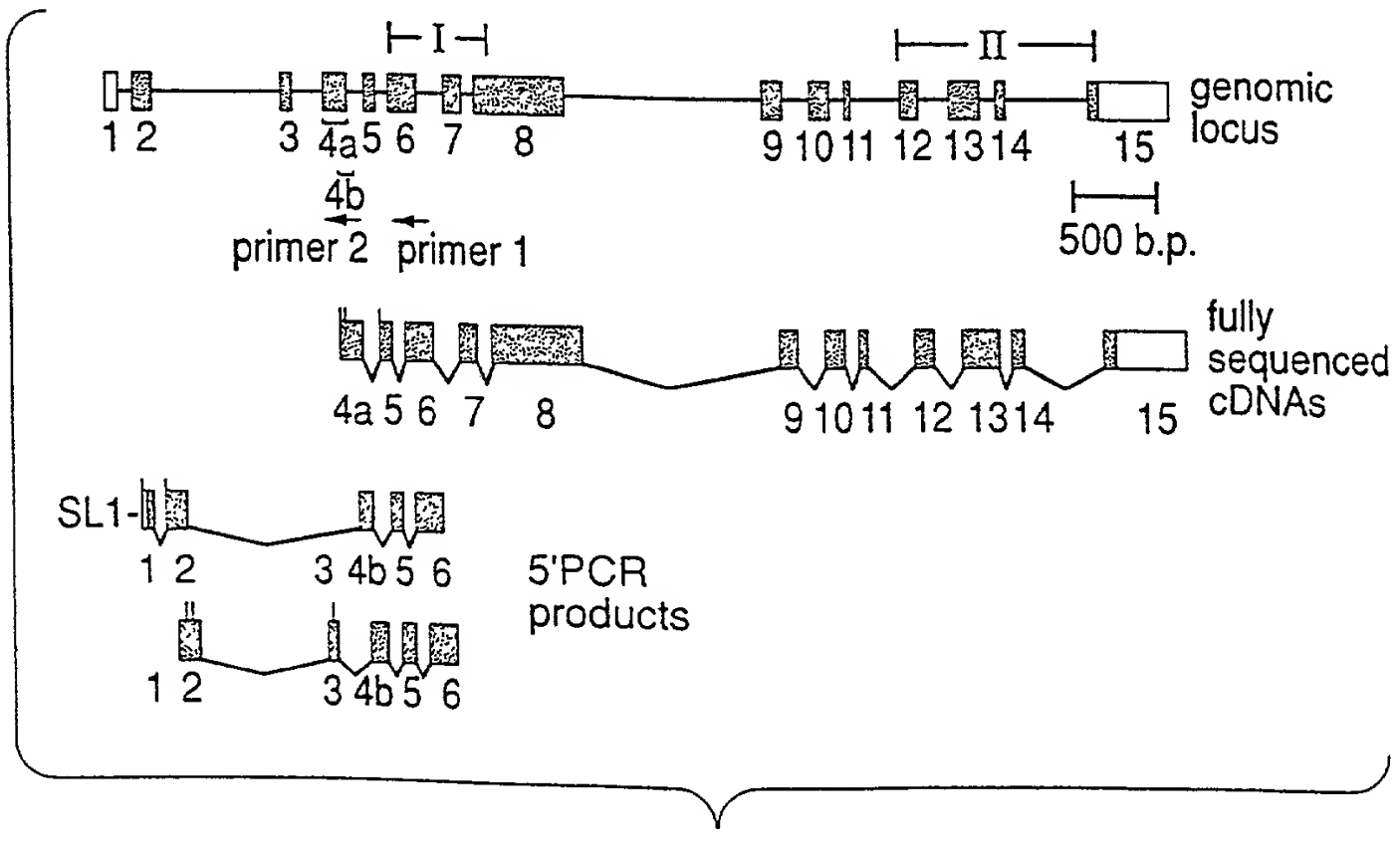
Fig. 5A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II
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genomic locus
4b
primer 2
primer 1
500 b.p.
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fully sequenced cDNAs
SL1-
1 2 3 4b 5 6
1 2 3 4b 5 6
5'PCR products

Fig. 5B

Domain I

```
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DPC4     GGESETFAKRAIESLVKKLKEKKDELDSLITAITTNGAHPSKCVTIQRTLDG
              mg125 P->L
         RLQVHGRKGFPHVVYGKLWRFNEMTKNETRHVDHCKHAFEMKSDMVCVNPYH
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Domain II

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DPC4     IAYFEMDVQVGETFKVPSSCPIVTVDGYVDPSGGDRFCLGQLSNVHRTEAIERA
         mg132  G->E
         RKAIVDGIRFSYKKDGSVWLQNRMKYPVFVTSGYLDEQSGGLKKDKVHKVYGCA
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         YIKVFDLRQCHRQMQQQAATAQAAAAAQAAAVAGNIPGPGSVGGIAPAISLSAA

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Fig. 5C

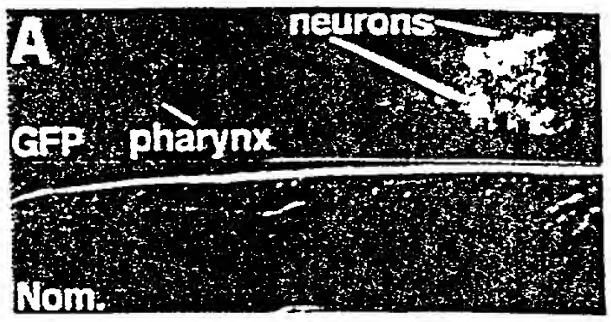


Fig. 6A

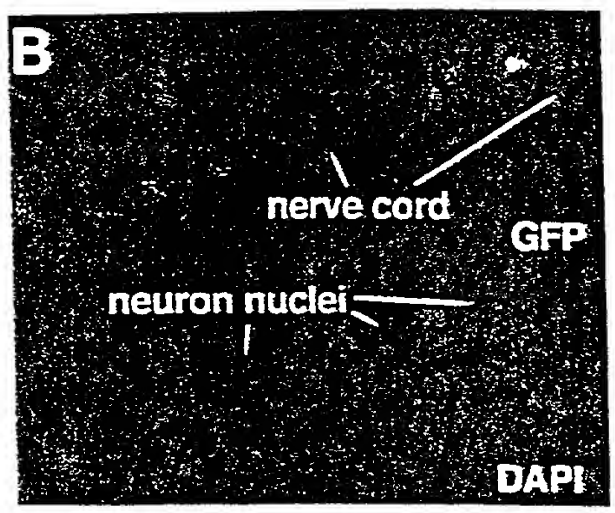


Fig. 6B

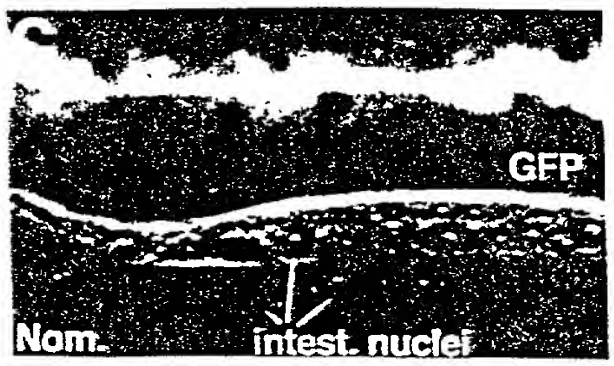


Fig. 6C

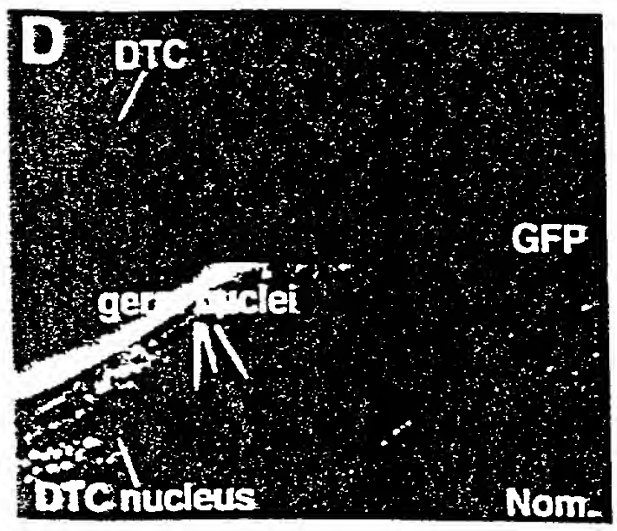


Fig. 6D

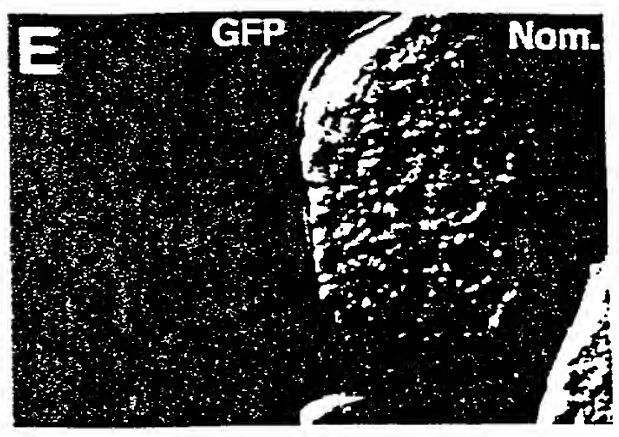


Fig. 6E

Fig. 6F

Fig. 6G

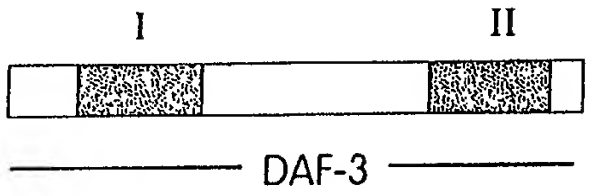
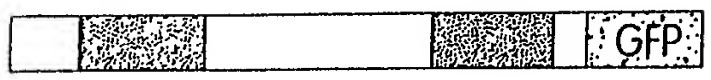
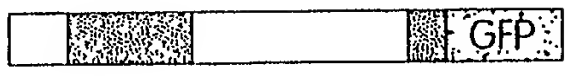
		Rescue of *daf-7; daf-3*	Suppression of *daf-7*
		dauer (i.e. rescued)	non-dauers (i.e. suppressed)
1		5 ± 1%	97 ± 3%
2		12 ± 3%	82 ± 6%
3		ND	90 ± 3%
4	Controls	0%	19 ± 4%

Fig. 7

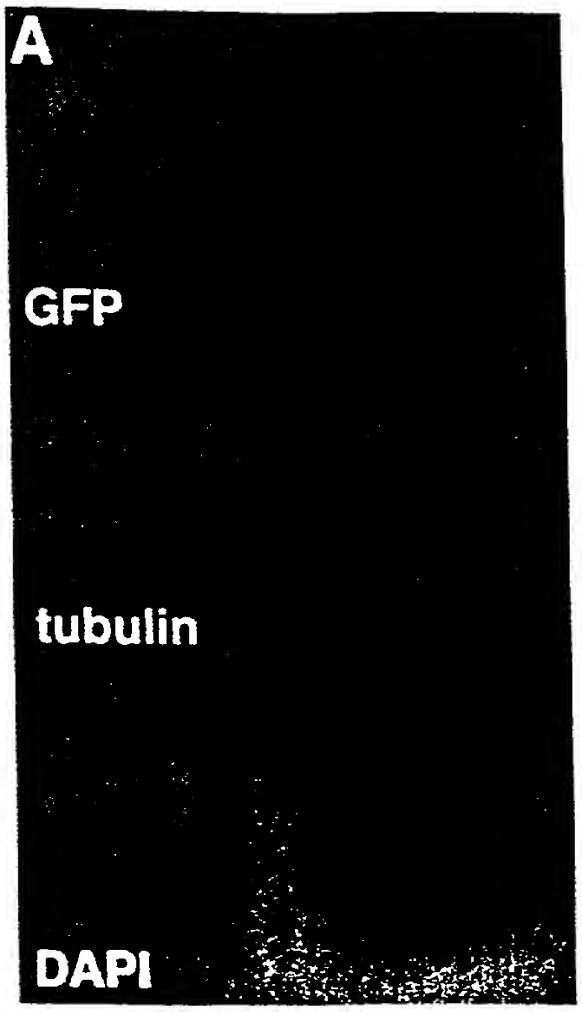

A
GFP
tubulin
DAPI

Fig. 8A

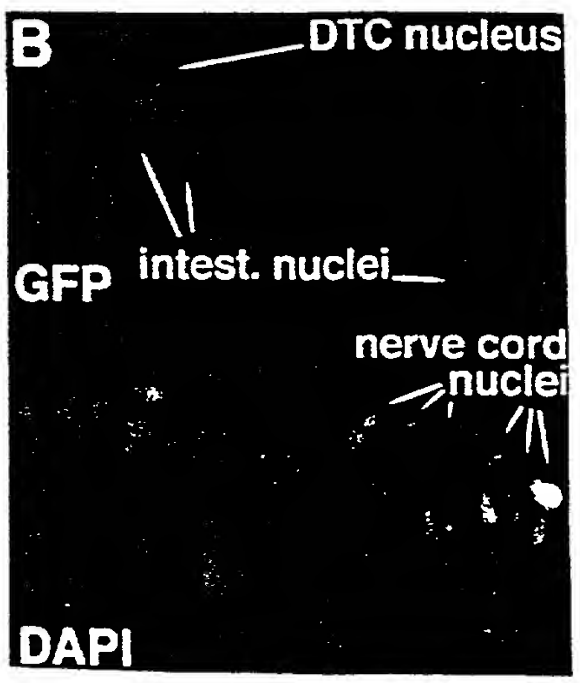

B
DTC nucleus
GFP
intest. nuclei
nerve cord nuclei
DAPI

Fig. 8B

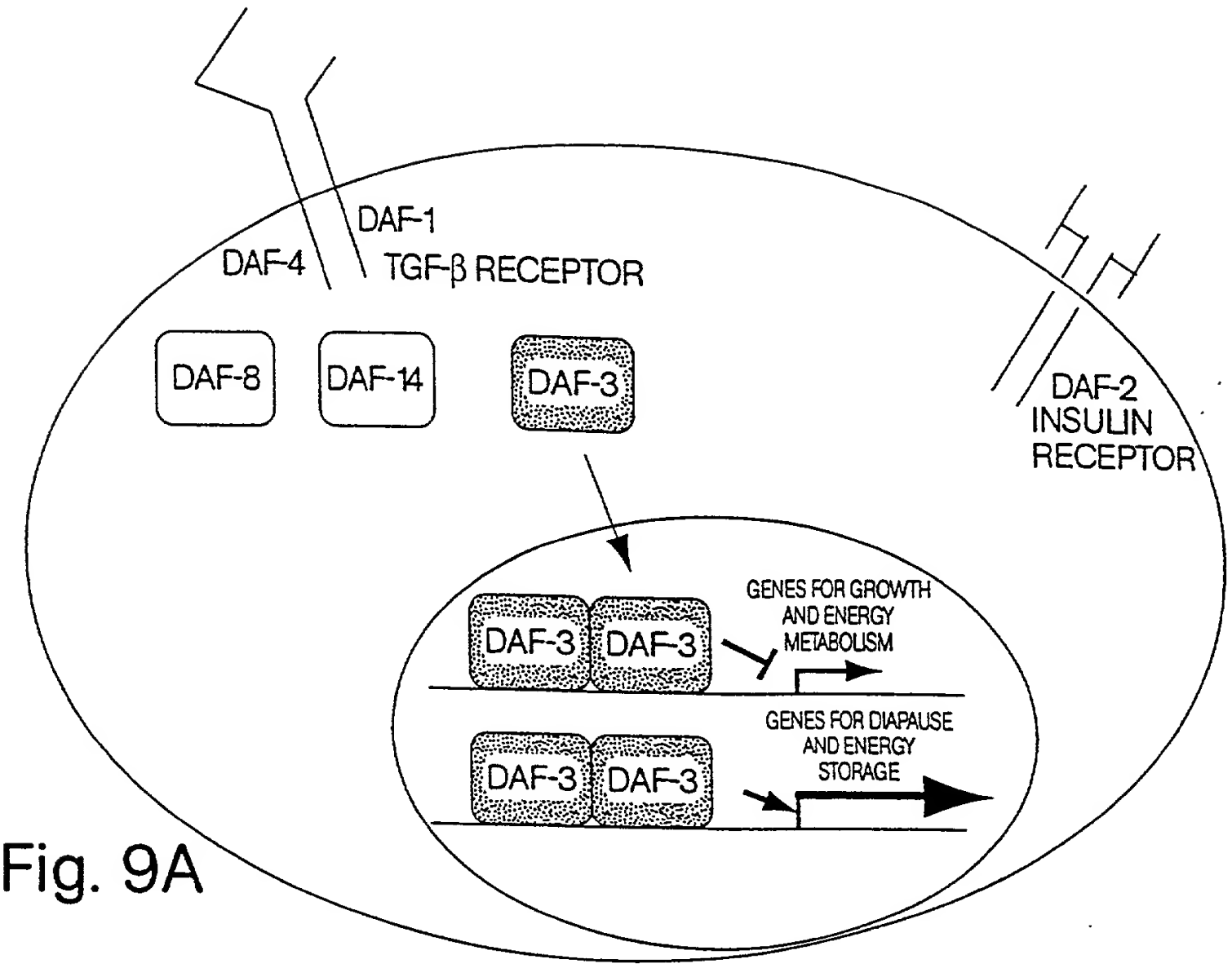

DAF-1
DAF-4
TGF-β RECEPTOR
DAF-8
DAF-14
DAF-3
DAF-2
INSULIN
RECEPTOR
DAF-3
DAF-3
GENES FOR GROWTH
AND ENERGY
METABOLISM
DAF-3
DAF-3
GENES FOR DIAPAUSE
AND ENERGY
STORAGE

Fig. 9A

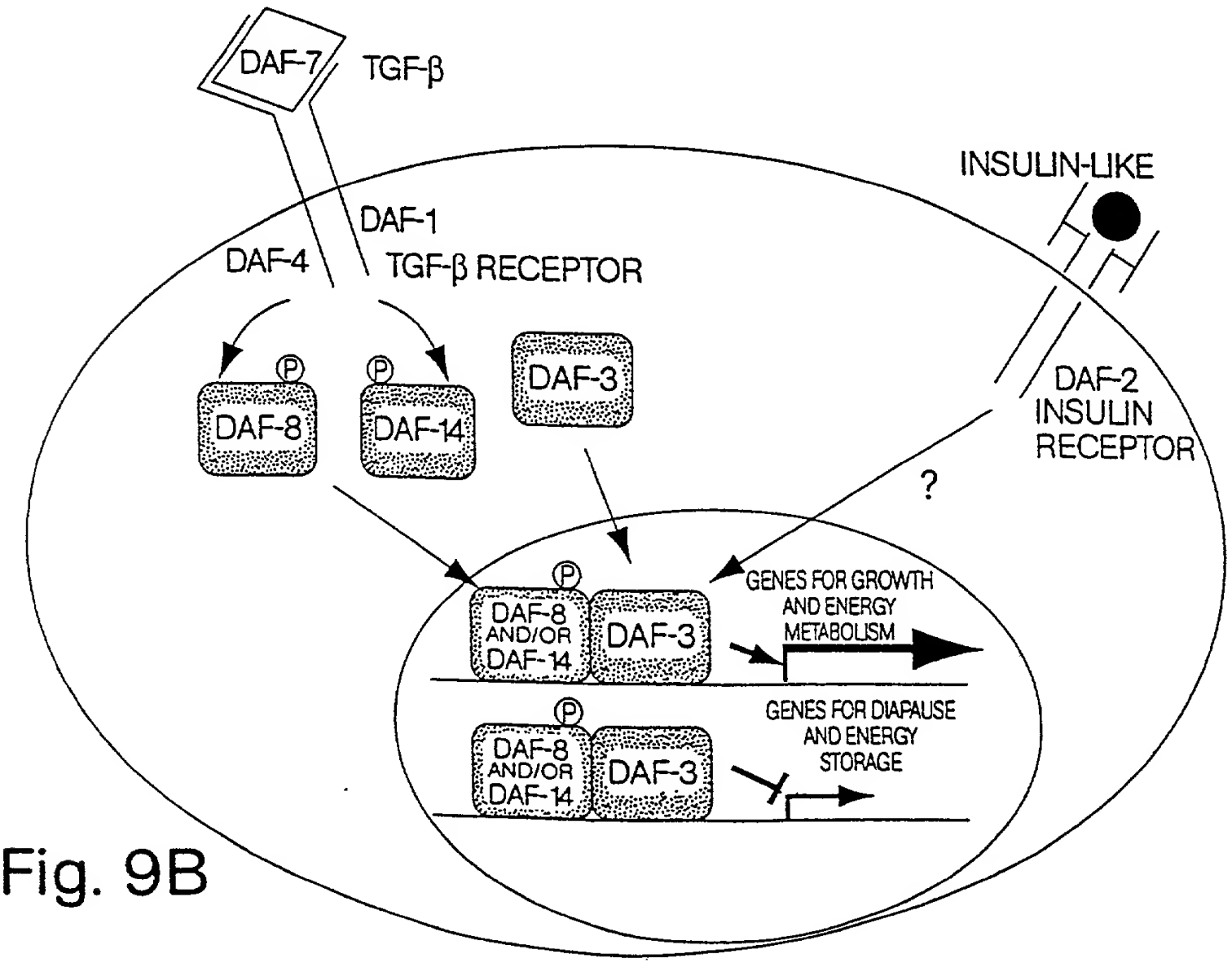

DAF-7
TGF-β
INSULIN-LIKE
DAF-1
DAF-4
TGF-β RECEPTOR
P
DAF-8
P
DAF-14
DAF-3
DAF-2
INSULIN
RECEPTOR
?
P
DAF-8
AND/OR
DAF-14
DAF-3
GENES FOR GROWTH
AND ENERGY
METABOLISM
P
DAF-8
AND/OR
DAF-14
DAF-3
GENES FOR DIAPAUSE
AND ENERGY
STORAGE

Fig. 9B

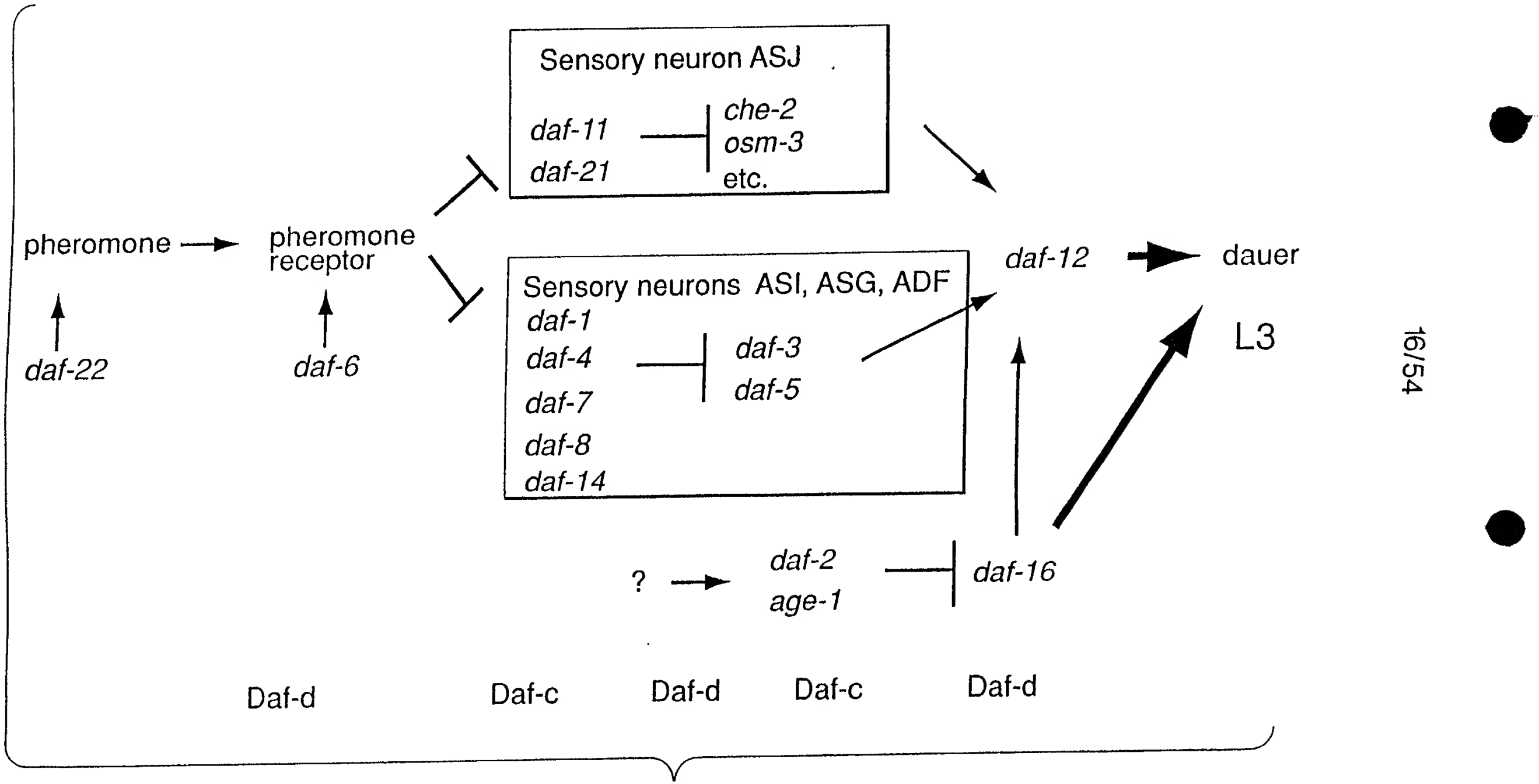

Sensory neuron ASJ
daf-11
daf-21
che-2
osm-3
etc.
pheromone
pheromone receptor
daf-22
daf-6
Sensory neurons ASI, ASG, ADF
daf-1
daf-4
daf-7
daf-8
daf-14
daf-3
daf-5
daf-12
dauer
L3
?
daf-2
age-1
daf-16
Daf-d
Daf-c
Daf-d
Daf-c
Daf-d

Fig. 10

```
   1  atgaagctaa tagcaacttc tcttctagtt cccgacgagc acacaccgat
  51  gatgtcacca gtgaatacaa ctacaaagat tctacaacgg agtggtatta
 101  aaatggaaat cccgccatat ttggatccag acagtcagga tgatgacccg
 151  gaagatggtg tcaactaccc ggatccagat ttatttgaca caaaaaacac
 201  aaatatgacc gagtacgatt tggatgtgtt gaagcttgga aaaccagcag
 251  tagatgaagc acggaaaaag atcgaagttc ccgacgctag tgcgccgcca
 301  aacaaaattg tagaatattt gatgtattat agaacgttaa aagaaagtga
 351  actcatacaa ctgaatgcgt atcggacaaa acgaaatcga ttatcgttga
 401  acttggtcaa aaacaatatt gatcgagagt tcgaccaaaa agcttgcgag
 451  tccctggtga aaaaattgaa ggataagaag aatgatctcc agaacctgat
 501  tgatgtggtt ctttcaaaag gtacaaaata taccggttgc attacaattc
 551  caaggacact tgatggccgg ttacaggtcc acggaagaaa aggtttccct
 601  cacgtagtct atggcaaact gtggaggttt aatgaaatga caaaaaacga
 651  aacgcgtcat gtggaccact gcaagcacgc atttgaaatg aaaagtgaca
 701  tggtatgcgt gaatccctat cactacgaaa ttgtcattgg aactatgatt
 751  gttgggcaga gggatcatga caatcgagat atgccgccgc cacatcaacg
 801  ctaccacact ccaggtcggc aggatccagt tgacgatatg agtagattta
 851  taccaccagc ttccattcgt ccgcctccga tgaacatgca cacaaggcct
 901  cagcctatgc ctcaacaatt gccttcagtt ggcgcaacgt ttgcccatcc
 951  tctcccacat caggcgccac ataacccagg ggtttcacat ccgtactcca
1001  ttgctccaca gacccattac ccgttgaaca tgaacccaat tccgcaaatg
1051  ccgcaaatgc cacaaatgcc accacctctc catcagggat atggaatgaa
1101  tgggccgagt tgctcttcag aaaacaacaa tccattccac caaaatcacc
1151  attataatga tattagccat ccaaatcact attcctacga ctgtggtccg
1201  aacttgtacg ggtttccaac tccttatccg gattttcacc atcctttcaa
1251  tcagcaacca caccagccgc cacaactatc acaaaaccat acgtcccaac
1301  aaggcagtca tcaaccaggg caccaaggtc aggtaccgaa tgatccacca
1351  atttcaagac cagtgttaca accatcaaca gtcaccttgg acgtgttccg
1401  tcggtactgt agacagacat ttggaaatcg atttttttgaa ggagaaagtg
1451  aacaatccgg cgcaataatt cggtctagta acaaattcat tgaagaattt
1501  gattcgccga tttgtggtgt gacagttgtt cgaccgcgga tgacagacgg
1551  tgaggttttg gagaacatca tgccggaaga tgcaccatat catgacattt
1601  gcaagttcat tttgaggctc acatcagaaa gtgtaacttt ctcaggagag
1651  gggccagaag ttagtgattt gaacgaaaaa tggggaacaa ttgtgtacta
1701  tgagaaaaat ttgcaaattg gcgagaaaaa atgttcgaga ggaaatttcc
1751  acgtggatgg cggattcatt tgctctgaga atcgttacag tctcggactt
1801  gagccaaatc caattagaga accagtggcg tttaaagttc gtaaagcaat
1851  agtggatgga attcgctttt cctacaaaaa agacgggagt gtttggcttc
1901  aaaaccgcat gaagtacccg gtatttgtca cttctgggta tctcgacgag
1951  caatcaggag gcctaaagaa ggataaagtg cacaaagttt acggatgtgc
2001  gtctatcaaa acgtttggct tcaacgtttc caaacaaatc atcagagacg
2051  cgcttctttc caagcaaatg gcaacaatgt acttgcaagg aaaattgact
```

Fig. 11A (sheet 1 of 2)

```
2101  ccgatgaatt atatctacga gaagaagact caggaagagc tgcgaaggga
2151  agcaacacgc accactgatt cattggccaa gtactgttgt gtccgtgtct
2201  cgttctgcaa aggatttgga gaagcatacc cagaacgccc gtcaattcat
2251  gattgtccag tttggattga gttgaaaatc aacattgcct acgatttcat
2301  ggattcaatc tgccagtaca taaccaactg cttcgagccg ctaggaatgg
2351  aagattttgc aaaattggga atcaacgtca gtgatgacta aatgataact
2401  tttttcactc accctactag atactgattt agtcttattc caaatcatcc
2451  aacgatatca aactttttcc tttgaacttt gcatactatg ttatcacaag
2501  ttccaagcag tttcaataca aacataggat atgttaacaa cttttgataa
2551  gaatcaagtt accaactgtt cattgtgagc tttgagctgt atagaaggac
2601  aatgtatccc atacctcaat ctttaatagt catcagtcac tggtcccgca
2651  ccaatttttt cgattcgcat atgtcatata ttgcaccgtg gcccttttta
2701  ttgtaacttt taatatattt tcttcccaac ttgtgaatat gattgatgaa
2751  ccaccatttt gagtaataaa tgtatttttt gtgg
```

Fig. 11A (sheet 2 of 2)

```
   1  gtaatcaaat tgtaaaggaa aaatattaat agtcagagta cacataaatg
  51  ggtgatcatc ataatttaac gggccttccc ggtacctcca tcccgccaca
 101  gttcaactat tctcagcccg gtaccagcac cggaggcccg ctttatggtg
 151  gaaaaccttc tcatggattg gaagatattc ctgatgtaga ggaatatgag
 201  aggaacctgc tcggggctgg agcaggtttt aatctgctca atgtaggaaa
 251  tatggctaat gttcccgacg agcacacacc gatgatgtca ccagtgaata
 301  caactacaaa gattctacaa cggagtggta ttaaaatgga aatcccgcca
 351  tatttggatc cagacagtca ggatgatgac ccggaagatg gtgtcaacta
 401  cccggatcca gatttatttg acacaaaaaa cacaaatatg accgagtacg
 451  atttggatgt gttgaagctt ggaaaaccag cagtagatga agcacggaaa
 501  aagatcgaag ttcccgacgc tagtgcgccg ccaaacaaaa ttgtagaata
 551  tttgatgtat tatagaacgt taaaagaaag tgaactcata caactgaatg
 601  cgtatcggac aaaacgaaat cgattatcgt tgaacttggt caaaaacaat
 651  attgatcgag agttcgacca aaaagcttgc gagtccctgg tgaaaaaatt
 701  gaaggataag aagaatgatc tccagaacct gattgatgtg gttctttcaa
 751  aaggtacaaa atataccggt tgcattacaa ttccaaggac acttgatggc
 801  cggttacagg tccacggaag aaaaggtttc cctcacgtag tctatggcaa
 851  actgtggagg tttaatgaaa tgacaaaaaa cgaaacgcgt catgtggacc
 901  actgcaagca cgcatttgaa atgaaaagtg acatggtatg cgtgaatccc
 951  tatcactacg aaattgtcat tggaactatg attgttgggc agagggatca
1001  tgacaatcga gatatgccgc cgccacatca acgctaccac actccaggtc
1051  ggcaggatcc agttgacgat atgagtagat ttataccacc agcttccatt
1101  cgtccgcctc cgatgaacat gcacacaagg cctcagccta tgcctcaaca
1151  attgccttca gttggcgcaa cgtttgccca tcctctccca catcaggcgc
1201  cacataaccc aggggtttca catccgtact ccattgctcc acagacccat
1251  tacccgttga acatgaaccc aattccgcaa atgccgcaaa tgccacaaat
1301  gccaccacct ctccatcagg gatatggaat gaatgggccg agttgctctt
1351  cagaaaacaa caatccattc caccaaaatc accattataa tgatattagc
1401  catccaaatc actattccta cgactgtggt ccgaacttgt acgggtttcc
1451  aactccttat ccggattttc accatccttt caatcagcaa ccacaccagc
1501  cgccacaact atcacaaaac catacgtccc aacaaggcag tcatcaacca
1551  gggcaccaag gtcaggtacc gaatgatcca ccaatttcaa gaccagtgtt
1601  acaaccatca acagtcacct tggacgtgtt ccgtcggtac tgtagacaga
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1701  attcggtcta gtaacaaatt cattgaagaa tttgattcgc cgatttgtgg
1751  tgtgacagtt gttcgaccgc ggatgacaga cggtgaggtt ttggagaaca
1801  tcatgccgga agatgcacca tatcatgaca tttgcaagtt cattttgagg
1851  ctcacatcag aaagtgtaac tttctcagga gaggggccag aagttagtga
1901  tttgaacgaa aaatggggaa caattgtgta ctatgagaaa aatttgcaaa
1951  ttggcgagaa aaaatgttcg agaggaaatt tccacgtgga tggcggattc
2001  atttgctctg agaatcgtta cagtctcgga cttgagccaa atccaattag
2051  agaaccagtg gcgtttaaag ttcgtaaagc aatagtggat ggaattcgct
```

Fig. 11B (sheet 1 of 2)

```
2101  tttcctacaa aaaagacggg agtgtttggc ttcaaaaccg catgaagtac
2151  ccggtatttg tcacttctgg gtatctcgac gagcaatcag gaggcctaaa
2201  gaaggataaa gtgcacaaag tttacggatg tgcgtctatc aaaacgtttg
2251  gcttcaacgt ttccaaacaa atcatcagag acgcgcttct ttccaagcaa
2301  atggcaacaa tgtacttgca aggaaaattg actccgatga attatatcta
2351  cgagaagaag actcaggaag agctgcgaag ggaagcaaca cgcaccactg
2401  attcattggc caagtactgt tgtgtccgtg tctcgttctg caaaggattt
2451  ggagaagcat acccagaacg cccgtcaatt catgattgtc cagtttggat
2501  tgagttgaaa atcaacattg cctacgattt catggattca atctgccagt
2551  acataaccaa ctgcttcgag ccgctaggaa tggaagattt tgcaaaattg
2601  ggaatcaacg tcagtgatga ctaaatgata acttttttca ctcaccctac
2651  tagatactga tttagtctta ttccaaatca tccaacgata tcaaactttt
2701  tcctttgaac tttgcatact atgttatcac aagttccaag cagtttcaat
2751  acaaacatag gatatgttaa caacttttga taagaatcaa gttaccaact
2801  gttcattgtg agctttgagc tgtatagaag gacaatgtat cccatacctc
2851  aatctttaat agtcatcagt cactggtccc gcaccaattt tttcgattcg
2901  catatgtcat atattgcacc gtggcccttt ttattgtaac ttttaatata
2951  ttttcttccc aacttgtgaa tatgattgat gaaccaccat tttgagtaat
3001  aaatgtattt tttgtgg
```

Fig. 11B (sheet 2 of 2)

```
   1  gtaatcaaat tgtaaaggaa aaatattaat agtcagagta cacataaatg
  51  ggtgatcatc ataatttaac gggccttccc ggtacctcca tcccgccaca
 101  gttcaactat tctcagcccg gtaccagcac cggaggcccg ctttatggtg
 151  gaaaaccttc tcatggattg gaagatattc ctgatgtaga ggaatatgag
 201  aggaacctgc tcggggctgg agcaggtttt aatctgctca atgtaggaaa
 251  tatggctaat gaatttaaac caataatcac attggacacg aaaccacctc
 301  gtgatgccaa caagtcattg gcattcaatg gcgggttgaa gctaatcact
 351  ccgaaaactg aagttcccga cgagcacaca ccgatgatgt caccagtgaa
 401  tacaactaca aagattctac aacggagtgg tattaaaatg gaaatcccgc
 451  catatttgga tccagacagt caggatgatg acccggaaga tggtgtcaac
 501  tacccggatc cagatttatt tgacacaaaa aacacaaata tgaccgagta
 551  cgatttggat gtgttgaagc ttggaaaacc agcagtagat gaagcacgga
 601  aaaagatcga agttcccgac gctagtgcgc cgccaaacaa aattgtagaa
 651  tatttgatgt attatagaac gttaaaagaa agtgaactca tacaactgaa
 701  tgcgtatcgg acaaaacgaa atcgattatc gttgaacttg gtcaaaaaca
 751  atattgatcg agagttcgac caaaaagctt gcgagtccct ggtgaaaaaa
 801  ttgaaggata agaagaatga tctccagaac ctgattgatg tggttctttc
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 901  gccggttaca ggtccacgga agaaaaggtt tccctcacgt agtctatggc
 951  aaactgtgga ggtttaatga aatgacaaaa aacgaaacgc gtcatgtgga
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1051  cctatcacta cgaaattgtc attggaacta tgattgttgg gcagagggat
1101  catgacaatc gagatatgcc gccgccacat caacgctacc acactccagg
1151  tcggcaggat ccagttgacg atatgagtag atttatacca ccagcttcca
1201  ttcgtccgcc tccgatgaac atgcacacaa ggcctcagcc tatgcctcaa
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1651  cagggcacca aggtcaggta ccgaatgatc caccaatttc aagaccagtg
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1851  ggtgtgacag ttgttcgacc gcggatgaca gacggtgagg ttttggagaa
1901  catcatgccg gaagatgcac catatcatga catttgcaag ttcattttga
1951  ggctcacatc agaaagtgta actttctcag gagaggggcc agaagttagt
2001  gatttgaacg aaaaatgggg aacaattgtg tactatgaga aaaatttgca
2051  aattggcgag aaaaaatgtt cgagaggaaa tttccacgtg gatggcggat
```

Fig. 11C (sheet 1 of 2)

```
2101  tcatttgctc tgagaatcgt tacagtctcg gacttgagcc aaatccaatt
2151  agagaaccag tggcgtttaa agttcgtaaa gcaatagtgg atggaattcg
2201  cttttcctac aaaaaagacg ggagtgtttg gcttcaaaac cgcatgaagt
2251  acccggtatt tgtcacttct gggtatctcg acgagcaatc aggaggccta
2301  aagaaggata aagtgcacaa agtttacgga tgtgcgtcta tcaaaacgtt
2351  tggcttcaac gtttccaaac aaatcatcag agacgcgctt ctttccaagc
2401  aaatggcaac aatgtacttg caaggaaaat tgactccgat gaattatatc
2451  tacgagaaga agactcagga agagctgcga agggaagcaa cacgcaccac
2501  tgattcattg gccaagtact gttgtgtccg tgtctcgttc tgcaaaggat
2551  ttggagaagc atacccagaa cgcccgtcaa ttcatgattg tccagtttgg
2601  attgagttga aaatcaacat tgcctacgat ttcatggatt caatctgcca
2651  gtacataacc aactgcttcg agccgctagg aatggaagat tttgcaaaat
2701  tgggaatcaa cgtcagtgat gactaaatga taacttttt cactcaccct
2751  actagatact gatttagtct tattccaaat catccaacga tatcaaactt
2801  tttcctttga actttgcata ctatgttatc acaagttcca agcagtttca
2851  atacaaacat aggatatgtt aacaactttt gataagaatc aagttaccaa
2901  ctgttcattg tgagctttga gctgtataga aggacaatgt atcccatacc
2951  tcaatcttta atagtcatca gtcactggtc ccgcaccaat tttttcgatt
3001  cgcatatgtc atatattgca ccgtggccct ttttattgta acttttaata
3051  tattttcttc ccaacttgtg aatatgattg atgaaccacc attttgagta
3101  ataaatgtat tttttgtgg
```

Fig. 11C (sheet 2 of 2)

```
  1  MKLIATSLLV PDEHTPMMSP VNTTTKILQR SGIKMEIPPY LDPDSQDDDP
 51  EDGVNYPDPD LFDTKNTNMT EYDLDVLKLG KPAVDEARKK IEVPDASAPP
101  NKIVEYLMYY RTLKESELIQ LNAYRTKRNR LSLNLVKNNI DREFDQKACE
151  SLVKKLKDKK NDLQNLIDVV LSKGTKYTGC ITIPRTLDGR LQVHGRKGFP
201  HVVYGKLWRF NEMTKNETRH VDHCKHAFEM KSDMVCVNPY HYEIVIGTMI
251  VGQRDHDNRD MPPPHQRYHT PGRQDPVDDM SRFIPPASIR PPPMNMHTRP
301  QPMPQQLPSV GATFAHPLPH QAPHNPGVSH PYSIAPQTHY PLNMNPIPQM
351  PQMPQMPPPL HQGYGMNGPS CSSENNNPFH QNHHYNDISH PNHYSYDCGP
401  NLYGFPTPYP DFHHPFNQQP HQPPQLSQNH TSQQGSHQPG HQGQVPNDPP
451  ISRPVLQPST VTLDVFRRYC RQTFGNRFFE GESEQSGAII RSSNKFIEEF
501  DSPICGVTVV RPRMTDGEVL ENIMPEDAPY HDICKFILRL TSESVTFSGE
551  GPEVSDLNEK WGTIVYYEKN LQIGEKKCSR GNFHVDGGFI CSENRYSLGL
601  EPNPIREPVA FKVRKAIVDG IRFSYKKDGS VWLQNRMKYP VFVTSGYLDE
651  QSGGLKKDKV HKVYGCASIK TFGFNVSKQI IRDALLSKQM ATMYLQGKLT
701  PMNYIYEKKT QEELRREATR TTDSLAKYCC VRVSFCKGFG EAYPERPSIH
751  DCPVWIELKI NIAYDFMDSI CQYITNCFEP LGMEDFAKLG INVSDD
```

Fig. 12A

```
  1 MGDHHNLTGL PGTSIPPQFN YSQPGTSTGG PLYGGKPSHG LEDIPDVEEY
 51 ERNLLGAGAG FNLLNVGNMA NVPDEHTPMM SPVNTTTKIL QRSGIKMEIP
101 PYLDPDSQDD DPEDGVNYPD PDLFDTKNTN MTEYDLDVLK LGKPAVDEAR
151 KKIEVPDASA PPNKIVEYLM YYRTLKESEL IQLNAYRTKR NRLSLNLVKN
201 NIDREFDQKA CESLVKKLKD KKNDLQNLID VVLSKGTKYT GCITIPRTLD
251 GRLQVHGRKG FPHVVYGKLW RFNEMTKNET RHVDHCKHAF EMKSDMVCVN
301 PYHYEIVIGT MIVGQRDHDN RDMPPPHQRY HTPGRQDPVD DMSRFIPPAS
351 IRPPPMNMHT RPQPMPQQLP SVGATFAHPL PHQAPHNPGV SHPYSIAPQT
401 HYPLNMNPIP QMPQMPQMPP PLHQGYGMNG PSCSSENNNP FHQNHHYNDI
451 SHPNHYSYDC GPNLYGFPTP YPDFHHPFNQ QPHQPPQLSQ NHTSQQGSHQ
501 PGHQGQVPND PPISRPVLQP STVTLDVFRR YCRQTFGNRF FEGESEQSGA
551 IIRSSNKFIE EFDSPICGVT VVRPRMTDGE VLENIMPEDA PYHDICKFIL
601 RLTSESVTFS GEGPEVSDLN EKWGTIVYYE KNLQIGEKKC SRGNFHVDGG
651 FICSENRYSL GLEPNPIREP VAFKVRKAIV DGIRFSYKKD GSVWLQNRMK
701 YPVFVTSGYL DEQSGGLKKD KVHKVYGCAS IKTFGFNVSK QIIRDALLSK
751 QMATMYLQGK LTPMNYIYEK KTQEELRREA TRTTDSLAKY CCVRVSFCKG
801 FGEAYPERPS IHDCPVWIEL KINIAYDFMD SICQYITNCF EPLGMEDFAK
851 LGINVSDD
```

Fig. 12B

```
  1 MGDHHNLTGL PGTSIPPQFN YSQPGTSTGG PLYGGKPSHG LEDIPDVEEY
 51 ERNLLGAGAG FNLLNVGNMA NEFKPIITLD TKPPRDANKS LAFNGGLKLI
101 TPKTEVPDEH TPMMSPVNTT TKILQRSGIK MEIPPYLDPD SQDDDPEDGV
151 NYPDPDLFDT KNTNMTEYDL DVLKLGKPAV DEARKKIEVP DASAPPNKIV
201 EYLMYYRTLK ESELIQLNAY RTKRNRLSLN LVKNNIDREF DQKACESLVK
251 KLKDKKNDLQ NLIDVVLSKG TKYTGCITIP RTLDGRLQVH GRKGFPHVVY
301 GKLWRFNEMT KNETRHVDHC KHAFEMKSDM VCVNPYHYEI VIGTMIVGQR
351 DHDNRDMPPP HQRYHTPGRQ DPVDDMSRFI PPASIRPPPM NMHTRPQPMP
401 QQLPSVGATF AHPLPHQAPH NPGVSHPYSI APQTHYPLNM NPIPQMPQMP
451 QMPPPLHQGY GMNGPSCSSE NNNPFHQNHH YNDISHPNHY SYDCGPNLYG
501 FPTPYPDFHH PFNQQPHQPP QLSQNHTSQQ GSHQPGHQGQ VPNDPPISRP
551 VLQPSTVTLD VFRRYCRQTF GNRFFEGESE QSGAIIRSSN KFIEEFDSPI
601 CGVTVVRPRM TDGEVLENIM PEDAPYHDIC KFILRLTSES VTFSGEGPEV
651 SDLNEKWGTI VYYEKNLQIG EKKCSRGNFH VDGGFICSEN RYSLGLEPNP
701 IREPVAFKVR KAIVDGIRFS YKKDGSVWLQ NRMKYPVFVT SGYLDEQSGG
751 LKKDKVHKVY GCASIKTFGF NVSKQIIRDA LLSKQMATMY LQGKLTPMNY
801 IYEKKTQEEL RREATRTTDS LAKYCCVRVS FCKGFGEAYP ERPSIHDCPV
851 WIELKINIAY DFMDSICQYI TNCFEPLGME DFAKLGINVS DD
```

Fig. 12C

tgatctttcaagccgaagcaatcaagacctcaaagccaatcaactctactcacttttcttcagaaccttaacttttttgtg
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Fig. 13A

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Fig. 13B

MMEMLVDQGTDASSSASTSTSSVSRFGADTFMNTPDDVMMNDDMEPIPRDR
CNTWPMRRPQLEPPLNSSPIIHEQIPEEDADLYGSNEQCGQLGGASSNGST
AMLHTPDGSNSHQTSFPSDFRMSESPDDTVSGKKTTTRRNAWGNMSYAELI
TTAIMASPEKRLTLAQVYEWMVQNVPYFRDKGDSNSSAGWKNSIRHNLSLH
SRFMRIQNEGAGKSSWWVINPDAKPGMNPRRTRERSNTIETTTKAQLEKSR
RGAKKRIKERALMGSLHSTLNGNSIAGSIQTISHDLYDDDSMQGAFDNVPS
SFRPRTQSNLSIPGSSSRVSPAIGSDIYDDLEFPSWVGESVPAIPSDIVDR
TDQMRIDATTHIGGVQIKQESKPIKTEPIAPPPSYHELNSVRGSCAQNPLL
RNPIVPSTNFKPMPLPGAYGNYQNGGITPINWLSTSNSSPLPGIQSCGIVA
AQHTVASSSALPIDLENLTLPDQPLMDTMDVDALIRHELSQAGGQHIHFDL

Fig. 14A

MQQYIYQESSATIPHHHLNQHNNPYHPMHPHHQLPHMQQLPQPLLNLNMTT
LTSSGSSVASSIGGGAQCSPCASGSSTAATNSSQQQQTVGQMLAASVPCSS
SGMTLGMSLNLSQGGGPMPAKKKRCRKKPTDQLAQKKPNPWGEESYSDIIA
KALESAPDGRLKLNEIYQWFSDNIPYFGERSSPEEAAGWKNSIRHNLSLHS
RFMRIQNEGAGKSSWWVINPDAKPGMNPRRTRERSNTIETTTKAQLEKSRR
GAKKRIKERALMGSLHSTLNGNSIAGSIQTISHDLYDDDSMQGAFDNVPSS
FRPRTQSNLSIPGSSSRVSPAIGSDIYDDLEFPSWVGESVPAIPSDIVDRT
DQMRIDATTHIGGVQIKQESKPIKTEPIAPPPSYHELNSVRGSCAQNPLLR
NPIVPSTNFKPMPLPGAYGNYQNGGITPINWLSTSNSSPLPGIQSCGIVAA
QHTVASSSALPIDLENLTLPDQPLMDTMDVDALIRHELSQAGGQHIHFDL

Fig. 14B

```
   1 cggaagccat ggagctcgag atctgattgc tggacacgga cggaactccg acgtatctcg
  61 cagatgcatg ttaacatttt acatccacaa ctgcaaacga tggtcgagca gtggcaaatg
 121 cgagaacgcc catcgctgga gaccgagaat ggcaaaggat cgctgctcct ggaaaatgaa
 181 ggtgtcgcag atatcatcac tatgtgtcca ttcggagaag ttattagtgt agtatttccg
 241 tggtttcttg caaatgtgcg aacatcgcta gaaatcaagc tatcagattt caaacatcaa
 301 cttttcgaat tgattgctcc gatgaagtgg ggaacatatt ccgtaaagcc acaggattat
 361 gtgttcagac agttgaataa tttcggcgaa attgaagtta tatttaacga cgatcaaccc
 421 ctgtcgaaat tagagctcca cggcactttc ccaatgcttt ttctctacca acctgatgga
 481 ataaacaggg ataaagaatt aatgagtgat ataagtcatt gtctaggata ctcactggat
 541 aaactggaag agagcctcga tgaggaactc cgtcaatttc gtgcttctct ctgggctcgt
 601 acgaagaaaa cgtgcttgac acgtggactt gagggtacca gtcactacgc gttccccgaa
 661 gaacagtact tgtgtgttgg tgaatcgtgc ccgaaagatt tggaatcaaa agtcaaggct
 721 gccaagctga gttatcagat gttttggaga aaacgtaaag cggaaatcaa tggagtttgc
 781 gagaaaatga tgaagattca aattgaattc aatccgaacg aaactccgaa atctctgctt
 841 cacacgtttc tctacgaaat gcgaaaattg gatgtatacg ataccgatga tcctgcagat
 901 gaaggatggt ttcttcaatt ggctggacgt accacgtttg ttacaaatcc agatgtcaaa
 961 cttacgtctt atgatggtgt ccgttcggaa ctggaaagct atcgatgccc tggattcgtt
1021 gttcgccgac aatcactagt cctcaaagac tattgtcgcc caaaaccact ctacgaacca
1081 cattatgtga gagcacacga acgaaaactt gctctagacg tgctcagcgt gtctatagat
1141 agcacaccaa aacagagcaa gaacagtgac atggttatga ctgattttcg tccgacagct
1201 tcactcaaac aagtttcact ttgggacctt gacgcgaatc ttatgatacg gcctgtgaat
1261 atttctggat tcgatttccc ggccgacgtg gatatgtacg ttcgaatcga attcagtgta
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1681 atgccgagtc aaggacaata cacatatctc gtcaagcacc gaagtacttg gacggaaact
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2641 cgccaggaca tgcttgttct tcaagttctc gaagttatgg ataacatctg gaaggctgca
```

Fig. 15 (sheet 1 of 2)

2701 aacattgatt gctgtttgaa cccgtacgca gttcttccaa tgggagaaat gattggaatt
2761 attgaagttg tgcctaattg taaaacaata ttcgagattc aagttggaac aggattcatg
2821 aatacagcag ttcggagtat tgatccttcg tttatgaata agtggattcg gaaacaatgc
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Fig. 15 (sheet 2 of 2)

10520.03956950

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 121 VFRQLNNFGE IEVIFNDDQP LSKLELHGTF PMLFLYQPDG INRDKELMSD ISHCLGYSLD
 181 KLEESLDEEL RQFRASLWAR TKKTCLTRGL EGTSHYAFPE EQYLCVGESC PKDLESKVKA
 241 AKLSYQMFWR KRKAEINGVC EKMMKIQIEF NPNETPKSLL HTFLYEMRKL DVYDTDDPAD
 301 EGWFLQLAGR TTFVTNPDVK LTSYDGVRSE LESYRCPGFV VRRQSLVLKD YCRPKPLYEP
 361 HYVRAHERKL ALDVLSVSID STPKQSKNSD MVMTDFRPTA SLKQVSLWDL DANLMIRPVN
 421 ISGFDFPADV DMYVRIEFSV YVGTLTLASK STTKVNAQFA KWNKEMYTFD LYMKDMPPSA
 481 VLSIRVLYGK VKLKSEEFEV GWVNMSLTDW RDELRQGQFL FHLWAPEPTA NRSRIGENGA
 541 RIGTNAAVTI EISSYGGRVR MPSQGQYTYL VKHRSTWTET LNIMGDDYES CIRDPGYKKL
 601 QMLVKKHESG IVLEEDEQRH VWMWRRYIQK QEPDLLIVLS ELAFVWTDRE NFSELYVMLE
 661 KWKPPSVAAA LTLLGKRCTD RVIRKFAVEK LNEQLSPVTF HLFILPLIQA LKYEPRAQSE
 721 VGMMLLTRAL CDYRIGHRLF WLLRAEIARL RDCDLKSEEY RRISLLMEAY LRGNEEHIKI
 781 ITRQVDMVDE LTRISTLVKG MPKDVATMKL RDELRSISHK MENMDSPLDP VYKLGEMIID
 841 KAIVLGSAKR PLMLHWKNKN PKSDLHLPFC AMIFKNGDDL RQDMLVLQVL EVMDNIWKAA
 901 NIDCCLNPYA VLPMGEMIGI IEVVPNCKTI FEIQVGTGFM NTAVRSIDPS FMNKWIRKQC
 961 GIEDEKKKSK KDSTKNPIEK KIDNTQAMKK YFESVDRFLY SCVGYSVATY IMGIKDRHSD
1021 NLMLTEDGKY VHIDFGHILG HGKTKLGIQR DRQPFILTEH FMTVIRSGKS VDGNSHELQK
1081 FKTLCVEAYE VMWNNRDLFV SLFTLMLGME LPELSTKADL DHLKKTLFCN GESKEEARKF
1141 FAGIYEEAFN GSWSTKTNWL FHAVKHY
```

Fig. 16

CONVERGENT TGF-β AND INSULIN SIGNALING ACTIVATE GLUCOSE-BASED METABOLISM GENES

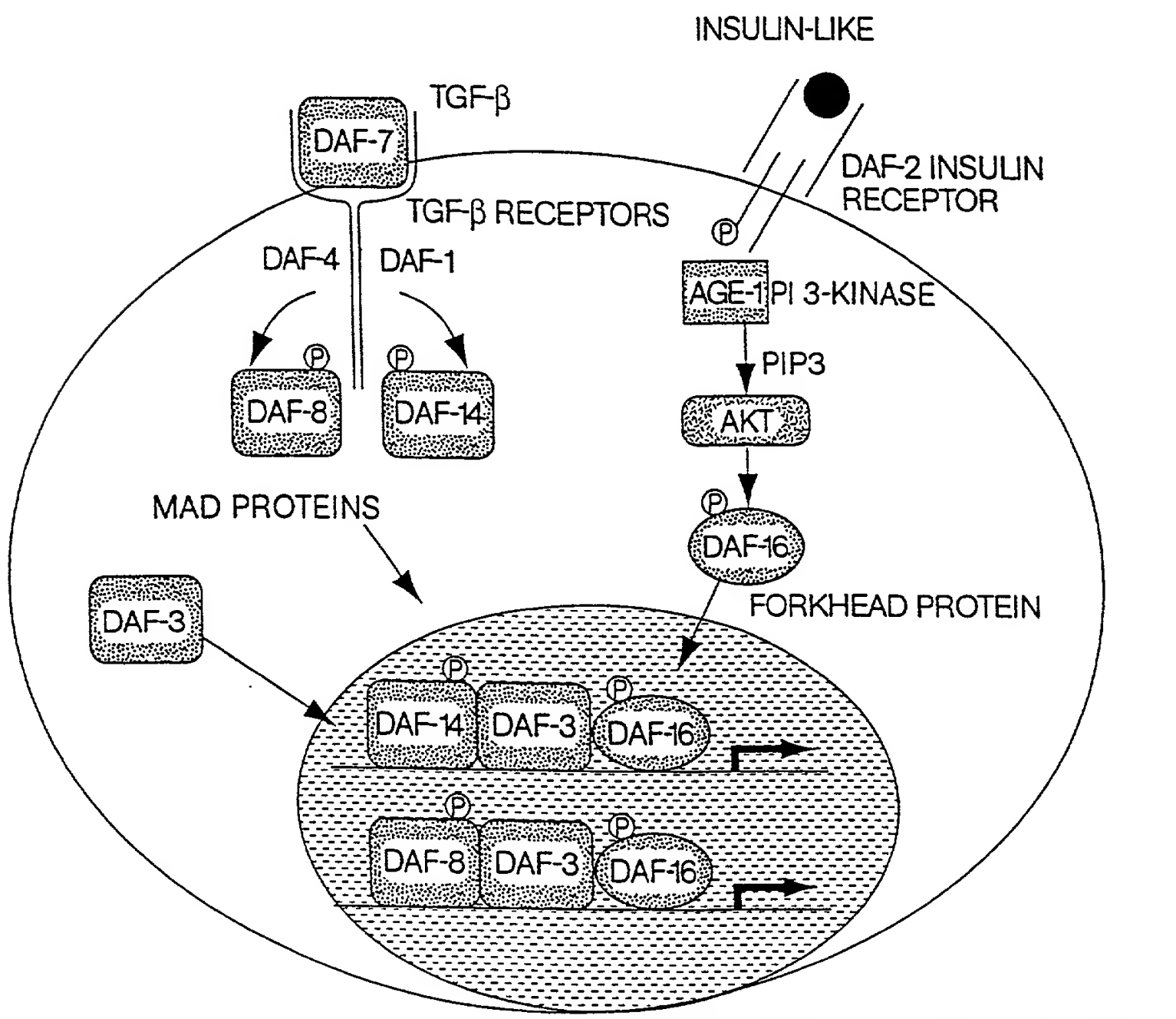
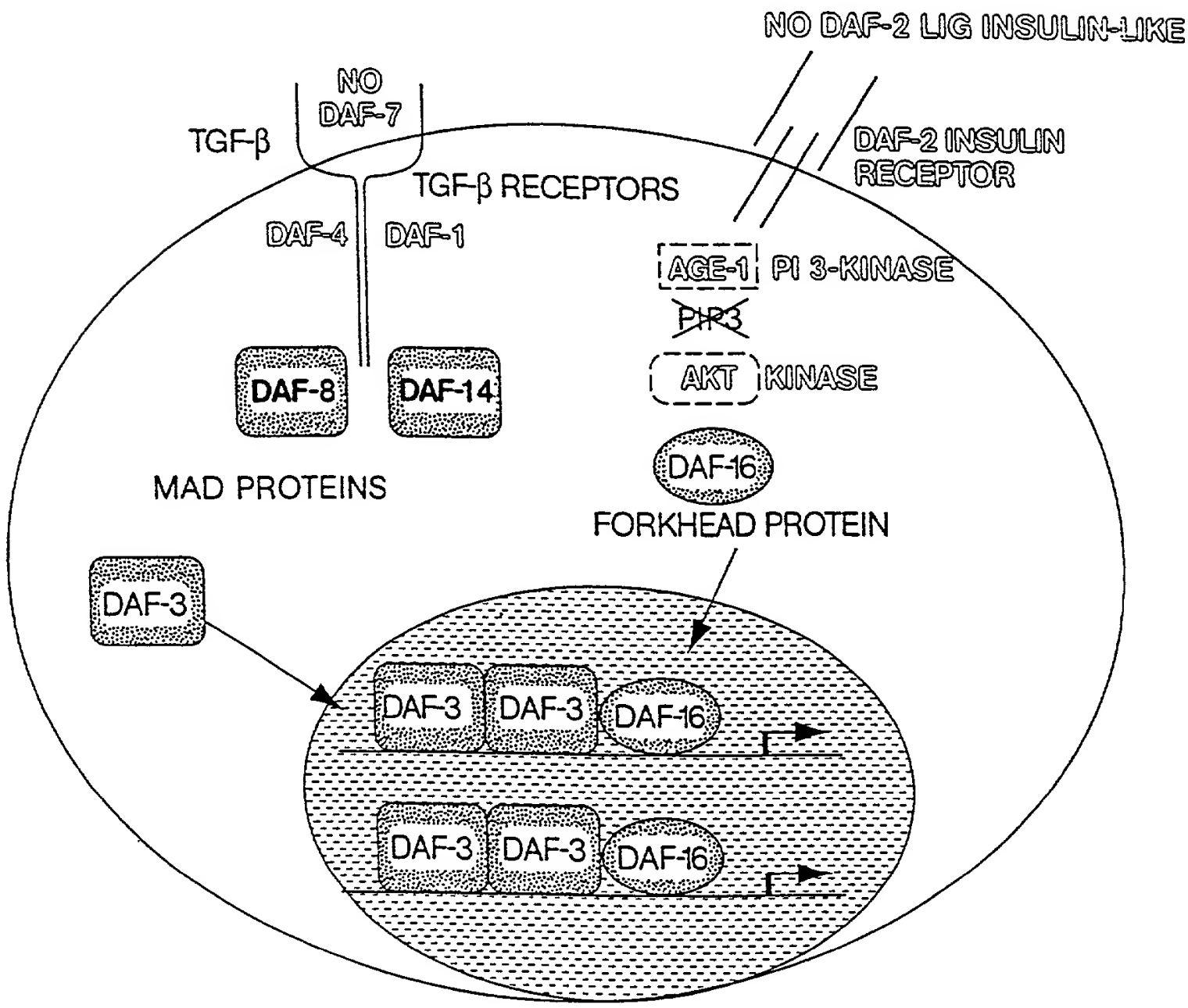


Fig. 17

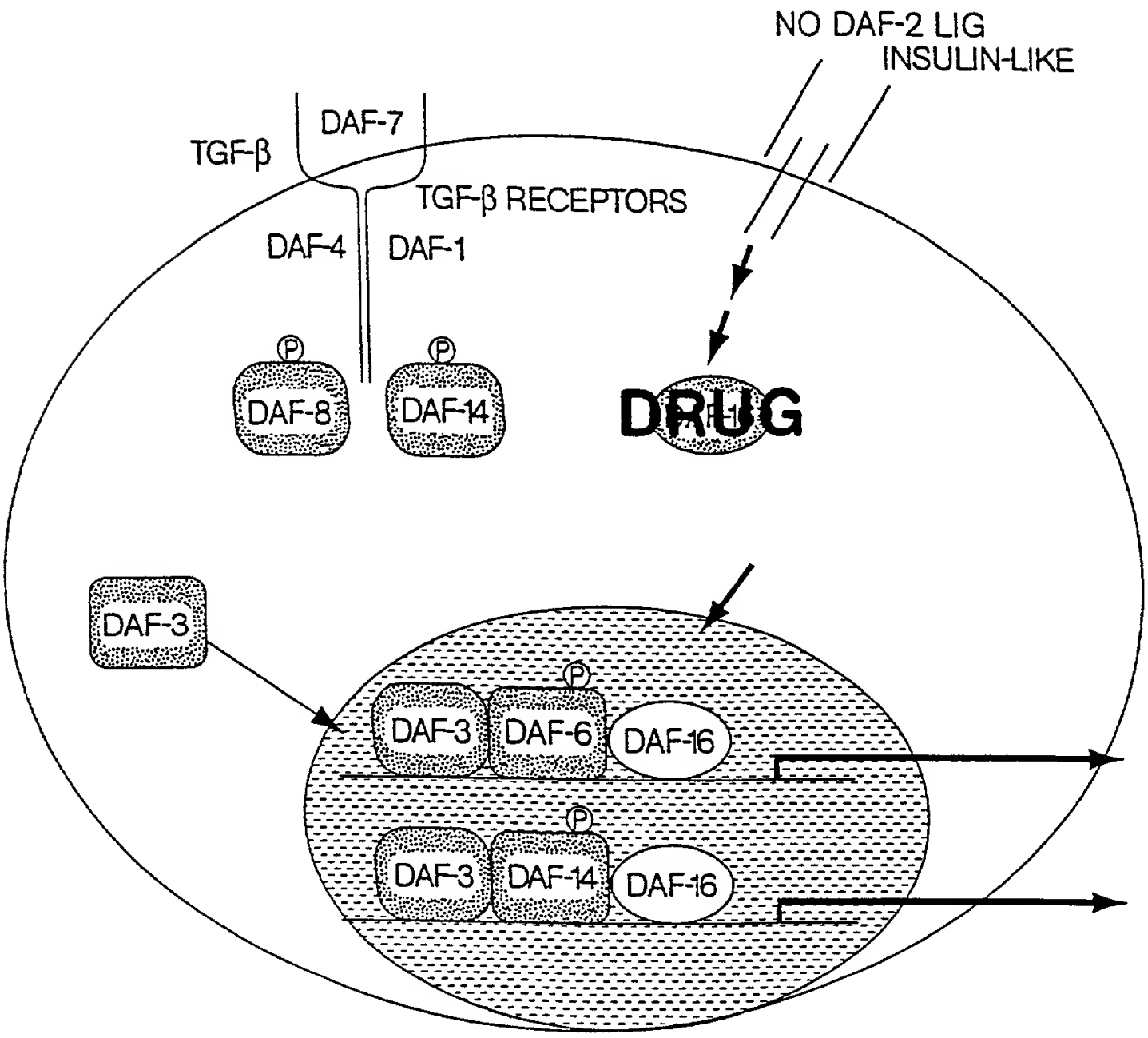
IN PHEROMONE, NO TGFβ OR INSULIN-LIKE SIGNALS CAUSES REPRESSION OF ANABOLIC GENES



REPRESS GLUCOSE BASED METABOLISM GENES
ACTIVE FAT METABOLISM

Fig. 18

**DRUGS THAT INHIBIT DAF-16 OR DAF-3
(OR PROTEINS IN THE PATHWAY)
CAN BE DISCOVERED USING REPORTER GENES
BEARING THEIR COGNATE BINDING SITES**



DRUG CAUSES A DECREASE IN DAF-16 ACTIVITY, ACTIVATING
THE REPORTER GENE LIKE A DAF-16 MUTANT.
THIS BYPASSES THE NEED FOR INSULIN

Fig. 19

DRUGS THAT INHIBIT DAF-3 WILL CURE THE DIABETES CAUSED BY A LACK OF DAF-7

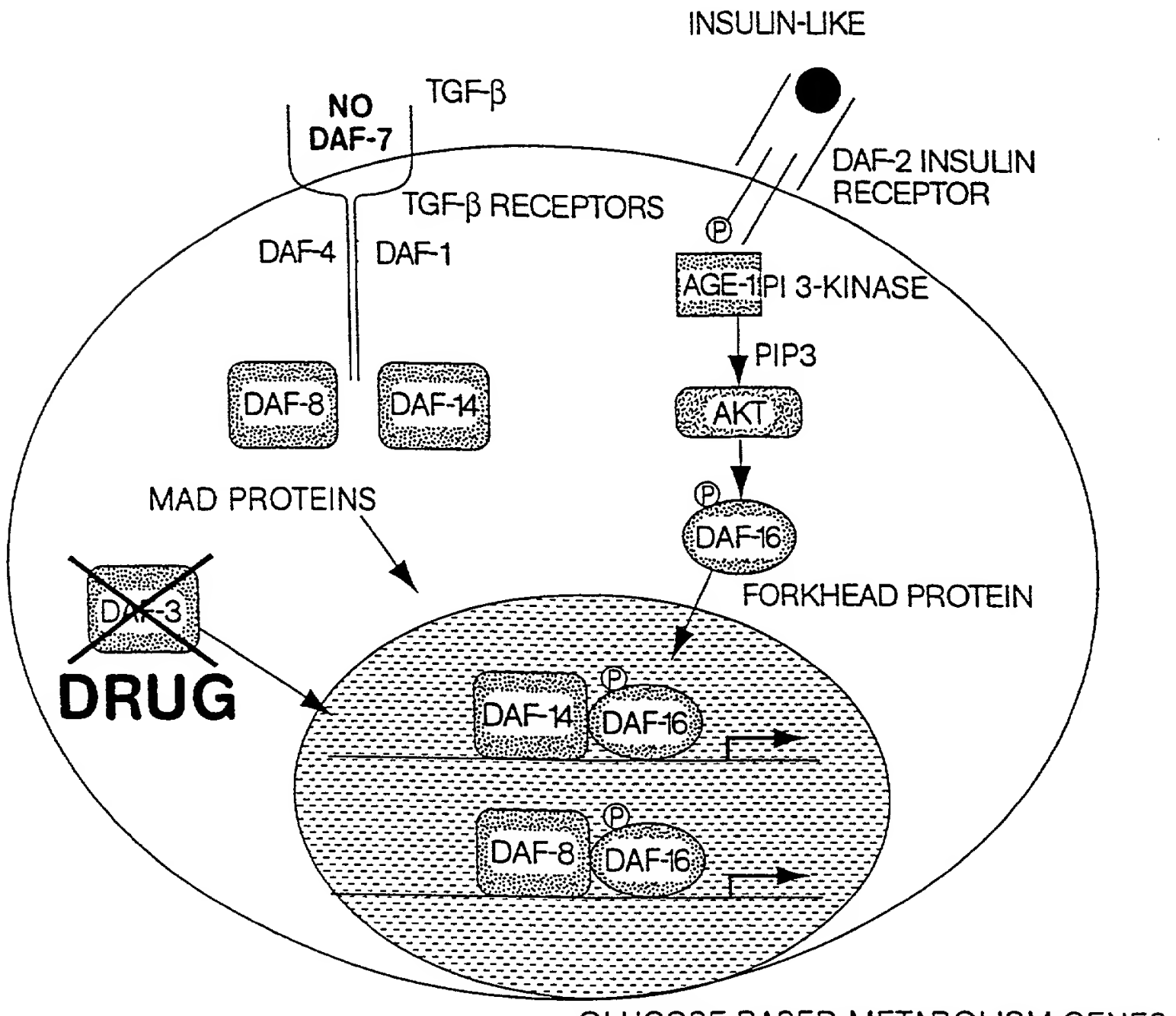


Fig. 20

```
DAF-16a1      1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~MMEMLVDQGTDASSSASTSTSSVSRFGADTFMNTPDDVMMNDDMEPIPRDR
DAF-16b       1 ~~~~~~~~~~~~~~~MNDSIDDDFPPEPRGRGYTWPMQQYIYQESSATIPHHHLNQHNNPYHPMHPHHQLPHMQQLPQPLLN
FKHR          1 ~~~~~~~~MAEAPQVVEIDPDFEPLPRPRSCTWPLPRPEFSQSNSATSSPAPSGSAAAN.........PDAAAGLPSASA
FKHRL1        1 MAEAPASPAPLSPLEVELDPEFEPQSRPRSCTWPLQRPELQASPAKPSGETAADSMIPE.........EEDDEDDEDGGG
AFX           1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~MRIQPQKAA

DAF-16a1     52 CN..TWPMRRPQLEPPLNSSPIIHEQIPEEDADLYGSNEQ...CGQLGGASSNGSTAMLHTPDGSNSHQTSFPSDFRMSE
DAF-16b      68 LNMTTLTSSGSSVASSIGGGAQCSPCASGSSTAATNSSQQQQTVGQMLAASVPCSSSGMTLGMSLNLSQGGGPMPAKKKR
FKHR         64 AAVSADFMSNLSLLEESEDFPQAPGSVAAAVAAAAAAAATGGLCGDFQGPEAGC.LHPAPPQPPPPGPLSQHPPVPPAAA
FKHRL1       72 RAGSAMAIGGGGGSGTLGSGLLLEDS..ARVLAPGGQDPGSGPATAAGGLSGGT.QALLQPQQPLP......PPQPGAAG
AFX          10 AIIDLDPDFEPQSRPRSCTWPLPRPEIANQPSEPPEVEPDLGEKVHTEGRSEPI.LLPSRLSEPAGGP...QPGILGAVT

DAF-16a1    127 SPDDTVSGKKTTTRRNAWGNMSYAELITTAIMASPEKRLTLAQVYEWMVQNVPYFRDKGDSNSSAGWKNSIRHNLSLHSR
DAF-16b     148 CRKKP.TDQLAQKKPNPWGEESYSDIIAKALESAPDGRLKLNEIYQWFSDNIPYFGERSSPEEAAGWKNSIRHNLSLHSR
FKHR        143 GPLAGQPRKSSSSRRNAWGNLSYADLITKAIESSAEKRLTLSQIYEWMVKSVPYFKDKGDSNSSAGWKNSIRHNLSLHSK
FKHRL1      143 GPLAGQPRKSSSSRRNAWGNLSYADLITRAIESSPDKRLTLSQIYEWMVRCVPYFKDKGDSNSSAGWKNSIRHNLSLHSR
AFX          86 G..SGQPRK.CSSRRNAWGNLSYADLITRAIESSPDKRLTLSQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSK
                GPRKG......GSRRNAWGNQSYAEFISQAIESAPEKRLTLAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSK

DAF-16a1    207 FMRIQNEGAGKSSWWVINPDAKPGRNPRRTRERSNTIETTTKAQLEKSRRGAKKRIKERALMGSLHSTLNGNSIAGSIQT
DAF-16b     227 FMRIQNEGAGKSSWWVINPDAKPGRNPRRTRERSNTIETTTKAQLEKSRRGAKKRIKERALMGSLHSTLNGNSIAGSIQT
FKHR        223 FIRVQNEGTGKSSWWMLNPEG..GKSGKSPRRRAASMDNNSKFAKSRSRAAKKK.......AS.LQSGQEGA.GDSPGSQ
FKHRL1      220 FMRVQNEGTGKSSWWIINPDG..GKSGKAPRRRAVSMDNSNKYTKSRGRAAKKK.......AA.LQTAPESA.DDSP.SQ
AFX         160 FIKVHNEATGKSSWWMLNPEG..GKSGKAPRRRAASMDSSSKLLRGRSKAPKKK.......PSVLPAPPEGATPTSPVGH

DAF-16a1    287 ISHDLYDDDSMQGAFDNVPSSFRPRTQSNLSIPGSSSRVSPAIGSDIYDDL.EFPSWVGESVPAIPSDIVDRTDQMRIDA
DAF-16b     307 ISHDLYDDDSMQGAFDNVPSSFRPRTQSNLSIPGSSSRVSPAIGSDIYDDL.EFPSWVGESVPAIPSDIVDRTDQMRIDA
FKHR        292 FSKWPASPGSHSNDDFDNWSTFRPRTSSNAS..TISGRLSPIM..TEQDDLGEGD..VHSMVYPPSAAKMAST.......
FKHRL1      288 LSKWPGSPTSRSSDELDAWTDFRSRTNSNAS..TVSGRLSPIMASTELDEVQDDDAPLSPMLYSSSASLSPSVSKPCTVE
AFX         231 FAKWSGSPCSRNREEADMWTTFRPRSSSNAS..SVSTRLSPLRPESEV.LAEEIPASVSSYAGGVPPTLNEGLELLDGLN

DAF-16a1    366 TTHIGGVQIKQESKPIKTEPIAPPPSYHELNSVRGSCAQNPLLRNPIVPSTNFKPMPLPGAYGNYQNGGITPINWLSTSN
DAF-16b     386 TTHIGGVQIKQESKPIKTEPIAPPPSYHELNSVRGSCAQNPLLRNPIVPSTNFKPMPLPGAYGNYQNGGITPINWLSTSN
FKHR        359 LPSLSEISNPENM.ENLLDNL.NLLSSPTSLTVSTQSSPGTMMQQTPCYSFAPP.NTSLNSPSPNYQKYTYGQSSMSPLP
FKHRL1      366 LPRLTDMAGTMNLNDGLTENLMDDLLDNITLPPSQPSPTGGLMQRSSSFPYTTK.GSGLGSPTSSFNSTVFGPSSLNSLR
AFX         308 LTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSSSLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVDPILS

DAF-16a1    446 SSPLPGIQS..CGIVAAQHTVASSSALPIDLENLTLPDQPLMDTMDVDALIRHELSQAGGQHIHFDL~~~~~~~~~~~~~~~
DAF-16b     466 SSPLPGIQS..CGIVAAQHTVASSSALPIDLENLTLPDQPLMDTMDVDALIRHELSQAGGQHIHFDL~~~~~~~~~~~~~~~
FKHR        436 QMPIQTLQDNK.SSYGGMSQYNCAPGLLKELLTSDSPPHNDI.MTPVDPGVAQPNSRVLGQNV...MMGPNSVMSTYGSQ
FKHRL1      445 QSPMQTIQENKPATFSSMSHY..GNQTLQDLLTSDSLSHSDVMMTQSDPLMSQASTAVSAQNSRRNVMLRNDPMMSFAAQ
AFX         388 QAPTLLLLGGLPSS....SKLATGVGLCPKPLEARGPSSLVPTLSMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMP

DAF-16a1    511 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
DAF-16b     531 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
FKHR        511 ASHNKMMNPSSH.THPGHAQQTSAVNGRPLPHTVSTMPHTSGMNRLTQVKTPVQVPLPHPMQMSALGGYSSVSSCNGYGR
FKHRL1      523 PNQGSLVN.QNL.LHHQHQTQGALGGSRALSNSVSNM.GLSESSSLGSAKHQQQSPVSQSMQ.TLSDSLSGSSLYSTSAN
AFX         464 QDLDLDMYMENLECDMDNIISDLMDEGEGLDFNFEPDP~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

FIG. 21A-1

```
DAF-16a1  511 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
DAF-16b   531 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
FKHR      590 MGLLHQEKLPSDLD.GMFIERLDCDMESIIRNDLMDGDTLDFNFDNVLPNQ........SFPHSVKTTTHSWVSG
FKHRL1    599 LPVMGHEKFPSDLDLDMFNGSLECDMESIIRSELMDADGLDFNFDSLISTQNVVGLNVGNFTGAKQASSQSWVPG
AFX       502 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

FIG. 21A-2

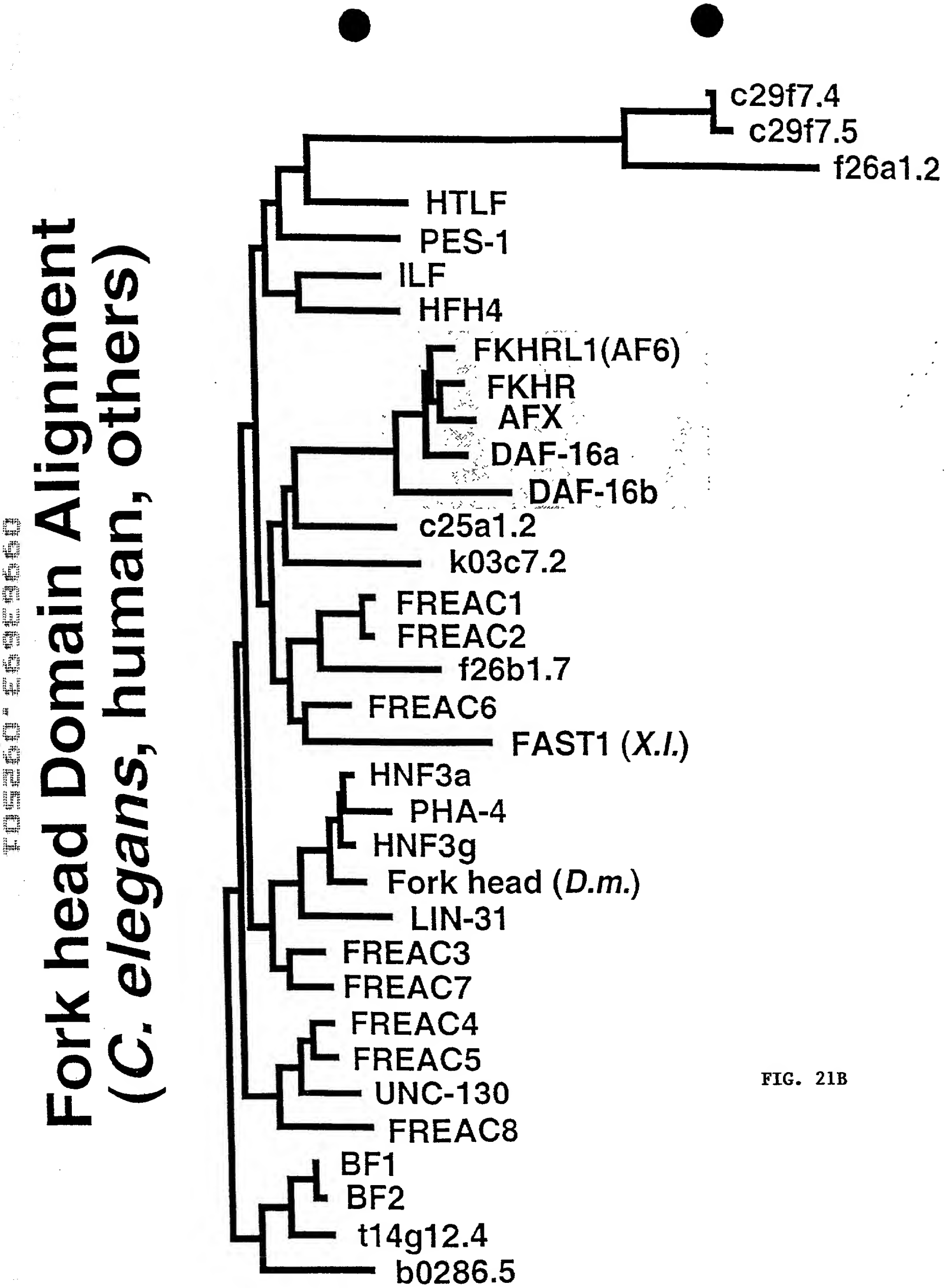

Fork head Domain Alignment
(C. elegans, human, others)
c29f7.4
c29f7.5
f26a1.2
HTLF
PES-1
ILF
HFH4
FKHRL1(AF6)
FKHR
AFX
DAF-16a
DAF-16b
c25a1.2
k03c7.2
FREAC1
FREAC2
f26b1.7
FREAC6
FAST1 (X.l.)
HNF3a
PHA-4
HNF3g
Fork head (D.m.)
LIN-31
FREAC3
FREAC7
FREAC4
FREAC5
UNC-130
FREAC8
BF1
BF2
t14g12.4
b0286.5

FIG. 21B

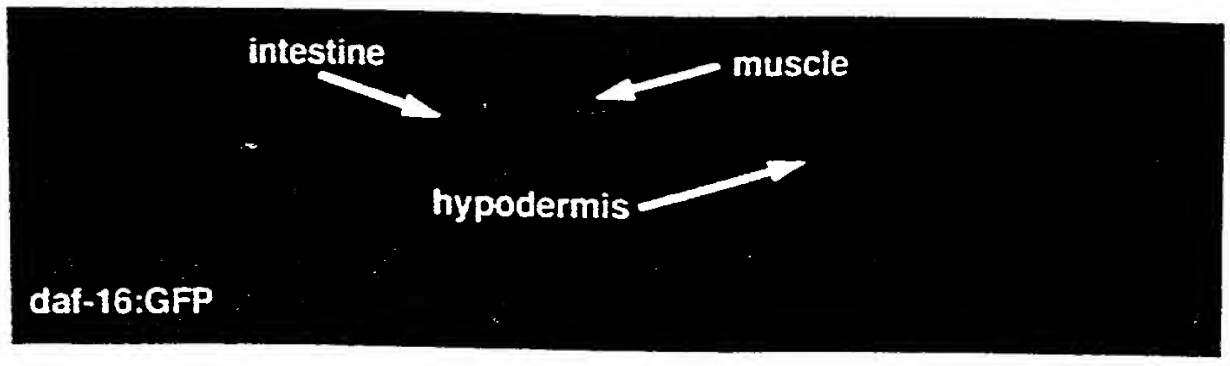
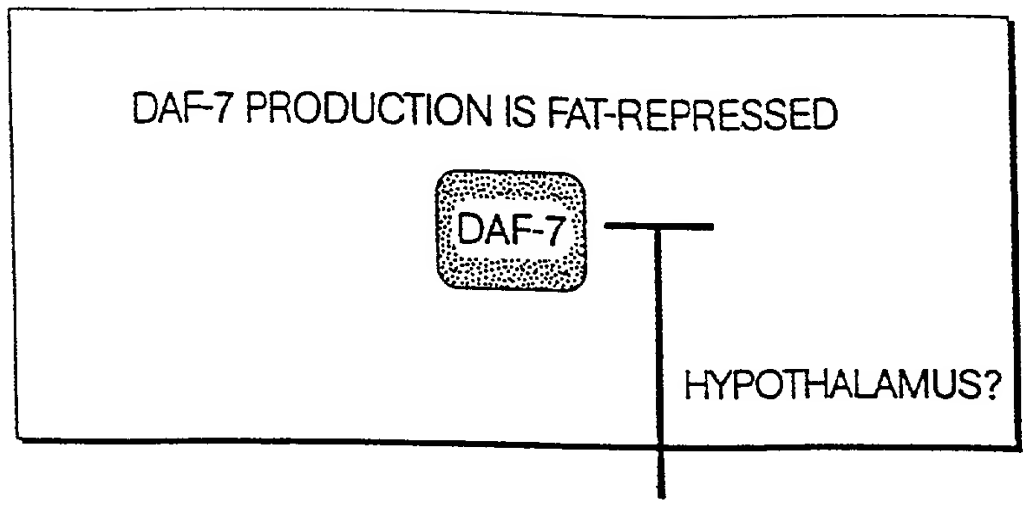


Fig. 22

INJECTION OF OF DAF-7 BYPASSES OBESITY-INDUCED DEFECTS IN INSULIN-REGULATION OF METABOLISM



FATTY ACIDS IN BLOOD REPRESS DAF-7 IN ANALOGY TO PHEROMONE REGULATION OF DAF-7 IN C. ELEGANS

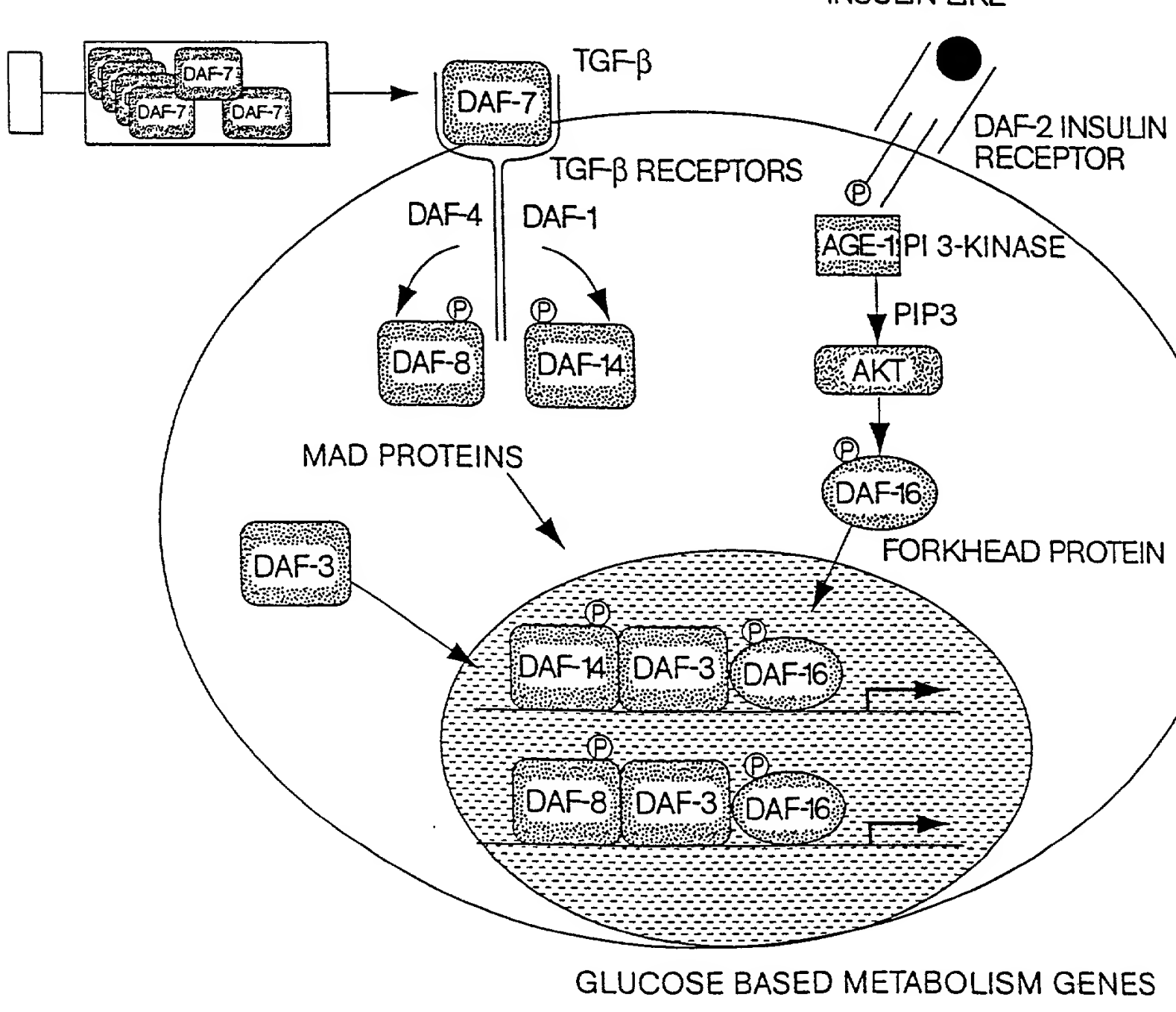


Fig. 23

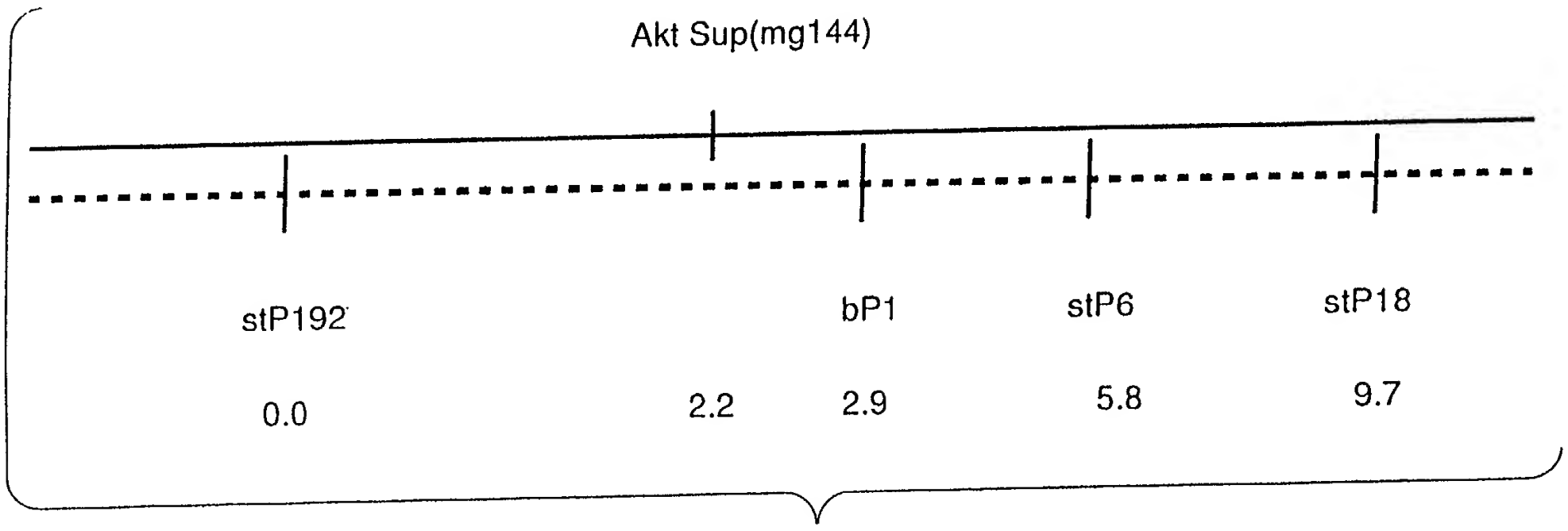


Fig. 24

Comparison of the human AKT protein sequence to the cosmid sequence C12D8, located in the genetic interval where sup(mg144) maps. Numbering in the AKT protein sequence by amino acid residues, and in the cosmid sequence by nucleotide position.

```
Score = 450 (207.4 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 79/121 (65%), Positives = 97/121 (80%), Frame = +1

Query:    319 EVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPEAKS 378
              +VL+D+DYGR VDWWG+GVVMYEMMCGRLPFY++DH KLFELI+  ++RFP  L  EA++
Sbjct:  33685 QVLDDHDYGRCVDWWGVGVVMYEMMCGRLPFYSKDHNKLFELIMAGDLRFPSKLSQEART 33864

Query:    379 LLSGLLKKDPTQRLGGGSEDAKEIMQHRFFANIVWQDVYEKKLSPPFKPQVTSETDTRYFD 439
              LL+GLL KDPTQRLGGG EDA EI +  FF  + W+  Y K++ PP+KP V SETDT YFD
Sbjct:  33865 LLTGLLVKDPTQRLGGGPEDALEICRADFFRTVDWEATYRKEIEPPYKPNVQSETDTSYFD 34047

Score = 256 (118.0 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 48/66 (72%), Positives = 59/66 (89%), Frame = +1

Query:    146 TMNEFEYLKLLGKGTFGKVILVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNS 205
              TM +F++LK+LGKGTFGKVIL KEK T + YA+KILKK+VI+A++EVAHTLTENRVLQ
Sbjct:  32314 TMEDFDFLKVLGKGTFGKVILCKEKRTQKLYAIKILKKDVIIAREEVAHTLTENRVLQRC 32493

Query:    206 RHPFLT 211
              +HPFLT
Sbjct:  32494 KHPFLT 32511

Score = 190 (87.6 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 36/45 (80%), Positives = 37/45 (82%), Frame = +2

Query:    276 KLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEV 320
              KLENL+LDKDGHIKI DFGLCKE I  G    TFCGTPEYLAPEV
Sbjct:  33509 KLENLLLDKDGHIKIADFGLCKEEISFGDKTSTFCGTPEYLAPEV 33643

Score = 188 (86.7 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 37/57 (64%), Positives = 42/57 (73%), Frame = +3

Query:    209 FLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLH 265
              +   LKYSFQ    LCFVM++ANGGELF H+ +   FSE RARFYGAEIV AL YLH
Sbjct:  32667 YFQELKYSFQEQHYLCFVMQFANGGELFTHVRKCGTFSEPRARFYGAEIVLALGYLH 32837

Score = 166 (76.5 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165
Identities = 29/59 (49%), Positives = 42/59 (71%), Frame = +1

Query:     53 NNFSVAQCQLMKTERPRPNTFIIRCLQWTTVIERTFHVETPEEREEWATAIQTVADGLK 111
              + F++   Q M  E+PRPN F++RCLQWTTVIERTF+ E+ E R+ W  AI++++   K
Sbjct:  31846 STFAIFYFQTMLFEKPRPNMFMVRCLQWTTVIERTFYAESAEVRQRWIHAIESISKKYK 32022

Score = 134 (61.8 bits), Expect = 5.2e-167, Sum P(8) = 5.2e-167
Identities = 24/33 (72%), Positives = 30/33 (90%), Frame = +3

Query:    210 LTALKYSFQTHDRLCFVMEYANGGELFFHLSRE 242
              L  LKYSFQT+DRLCFVME+A GG+L++HL+RE
Sbjct:  33156 LQELKYSFQTNDRLCFVMEFAIGGDLYYHLNRE 33254
```

Fig. 25

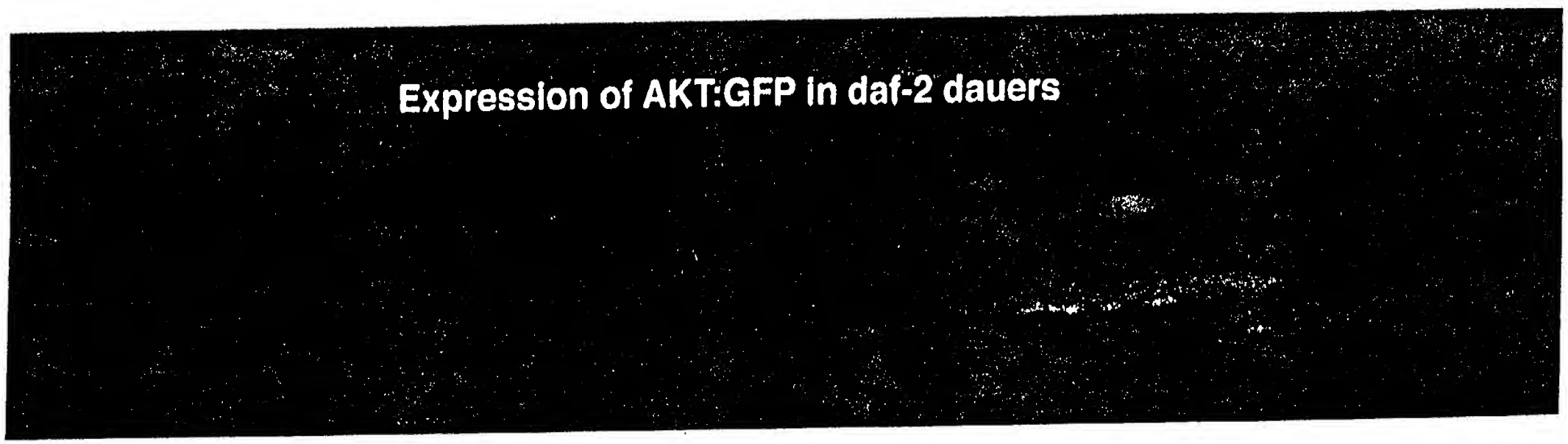


Fig. 26A

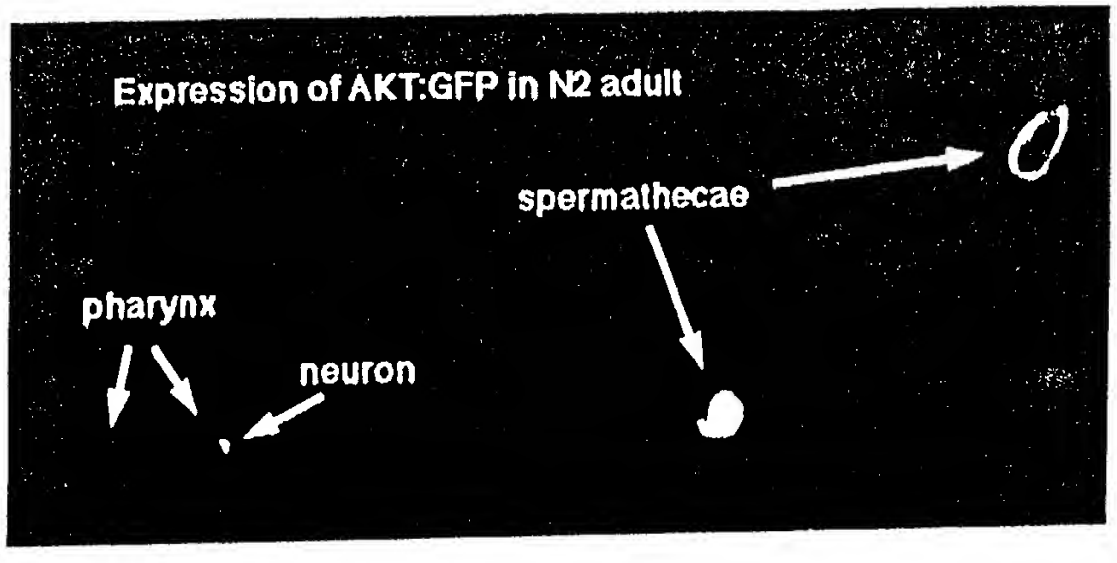


Fig. 26B

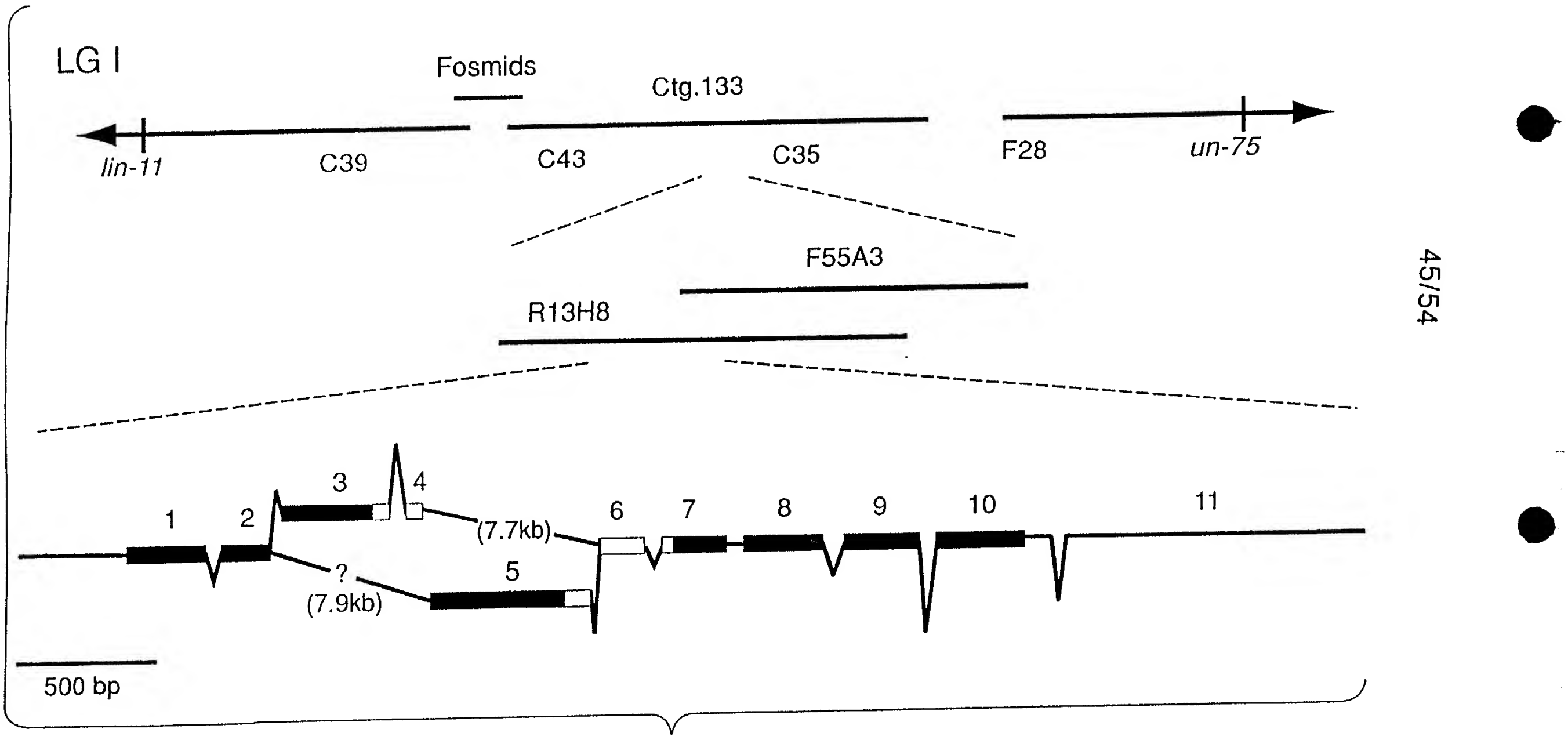

LG I
Fosmids
Ctg.133
lin-11
C39
C43
C35
F28
un-75
F55A3
R13H8
1
2
3
4
5
6
7
8
9
10
11
(7.7kb)
?
(7.9kb)
500 bp

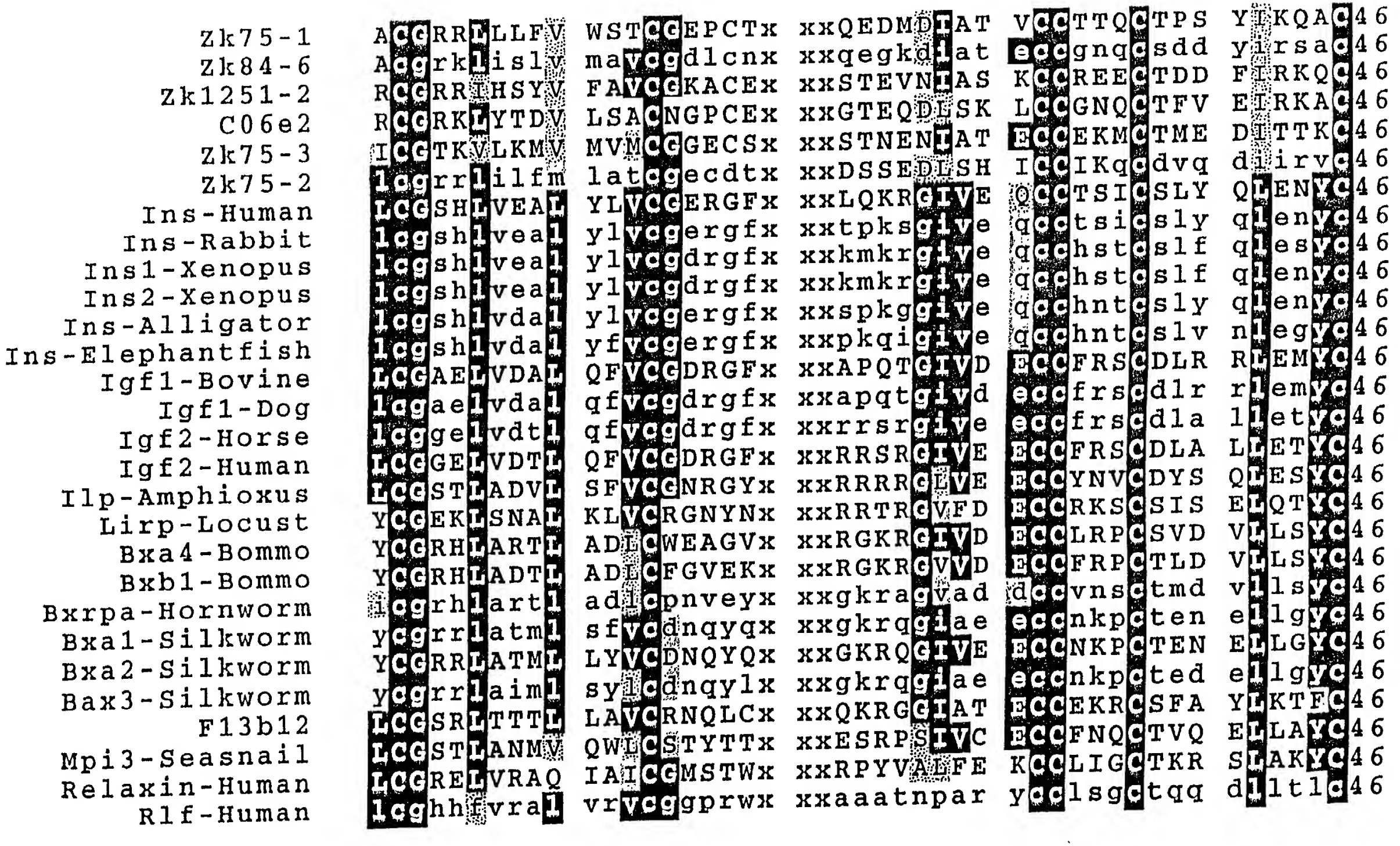
Fig. 27

```
                1               15 16              30 31              45 46              60
1 ZK84.6    -MNSVFTIIFVLCAL QVAASFRQSFG---P SMSEESASMQLLREL QH--NMMESAHRPMP   54
2 ZK75.1    -MFSFFT-YFLLSAL LLSASCRQ------P SMDT-SKADRILREI E----METELENQLS   47
3 ZK1251.2 ----MPPIILVFFLV LIPASQQY------P FSLE-SLNDQIINEE VI--EYMLENSIRSS   47
4 C06E2     --MIVTLIVFLVIGL QMAHLSQVSGNNENG FLNP-FDLSQWSEEI LHRQYHHHHHHHGN   57
5 ZK75.2    ----MNAIIFCLLFT TVTATYEVF-----G KGIEHRNEHLIINQL D---IIPVESTPTPN   48
6 ZK75.3    MKLSVVLALFIIFQL GAASLMRN------W MFDFEKELEHDYDDS E---IGFHNIHSLMA   51
7 C17C3     --------------- --------------- ---------MKLLHI F---IIFLLFQSCSN   18
8 F13E12    --------------- --------------- ----MYWFRQVYRPS FF--FGFLAILLLSS   50
9 INSULIN   --------------- --------------- ------------MA LWMRLLPLLALLALW   17
CONSENSUS   --------------- --------------- --------------- ---------------

                61              75 76              90 91             105 106            120
1 ZK84.6    RARRVPAPGETRACG RKLISLVMAVCGD-L CN------------- ---------------   85
2 ZK75.1    RARRVPA-GEVRACG RRLLLFVWSTCGE-P CT------------- ---------------   77
3 ZK1251.2 RTRRVPDEKKIYRCG RRIHSYVFAVCGK-A CE------------- ---------------   78
4 C06E2     RARRTLETEKIYRCG RKLYTDVLSACNG-P CE------------- ---------------   88
5 ZK75.2    RASRVQK----RLCG RRLILFMLATCG--E CD------------- ---------------   74
6 ZK75.3    RSRRGDK---VKICG TKVLKMVMVMCGG-E CS------------- ---------------   79
7 C17C3     KMCQYSK-KKYKICG VRALKHMKVYCTR-G MT------------- ---------------   48
8 F13E12    PTPSDAS---IRLCG SRLTTTLLAVCRNQL CTGLTAFKRSADQSY APTTRDLFHIHHQQ-   80
9 INSULIN   GPDPAAAFVNQHLCG SHLVEALYLVCGERG FFYTPKTRREAEDLQ VGQVELGGGPGAGSL   77
CONSENSUS   -------------CG -----------C---- ---------------  ---------------
                                  B CHAIN                          C PEPTIDE

                121         135 136         150 151        165 166          180
1 ZK84.6    -------PQEGKDIA TECCGNQCSDDYIRS ACCP-----    112
2 ZK75.1    -------PQEDMDIA TVCCTTQCTPSYIKQ ACCPEK---    106
3 ZK1251.2 -------SNTEVNIA SKCCREECTDDFIRK QCCP-----    105
4 C06E2     -------PGTEQDLS KLCCGNQCTFVEIRK ACCADKL--    118
5 ZK75.2    -------TDSSEDLS HICCIKQCDVQDIIR VCCPNSFRK    106
6 ZK75.3    -------S-TNENIA TECCEKMCTMEDITT KCCPSR---    107
7 C17C3     -------R-DYGKLL VTCCSKGCNAIDIQR ICL------     73
8 F13E12    ---------KRGGIA TECCEKRCSFAYLKT FCCNQDDN-    109
9 INSULIN   QPLALEGSLQKRGIV EQCCTSICSLYQLEN YCN-------    110
CONSENSUS   ------------------CC---C------- --C-------
                                  A CHAIN
```

Fig. 28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Zk1251-2
C06e2
Zk75-3
Zk75-2
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Ins-Rabbit
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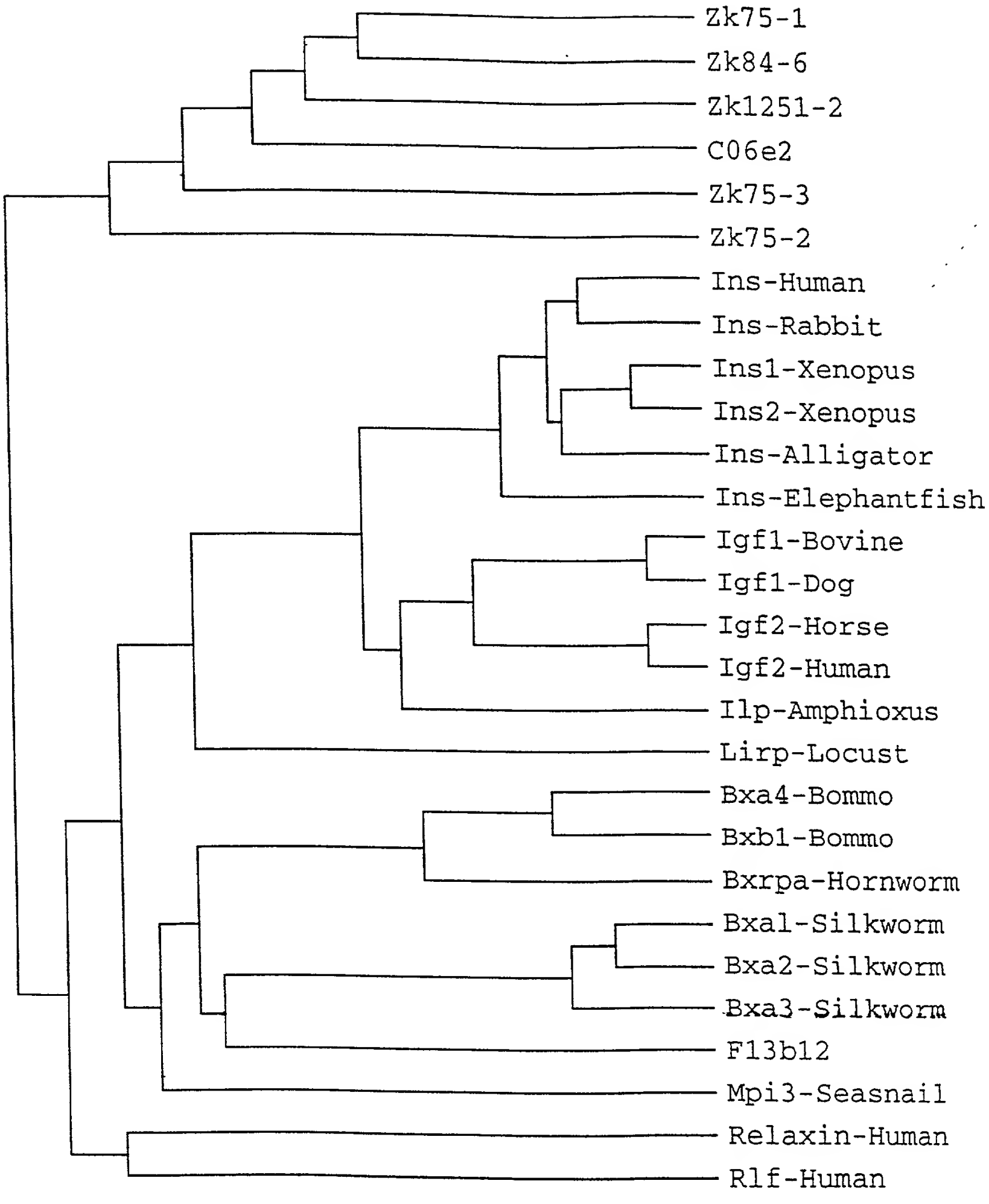
Ins2-Xenopus
Ins-Alligator
Ins-Elephantfish
Igf1-Bovine
Igf1-Dog
Igf2-Horse
Igf2-Human
Ilp-Amphioxus
Lirp-Locust
Bxa4-Bommo
Bxb1-Bommo
Bxrpa-Hornworm
Bxa1-Silkworm
Bxa2-Silkworm
Bax3-Silkworm
F13b12
Mpi3-Seasnail
Relaxin-Human
R1f-Human

Fig. 29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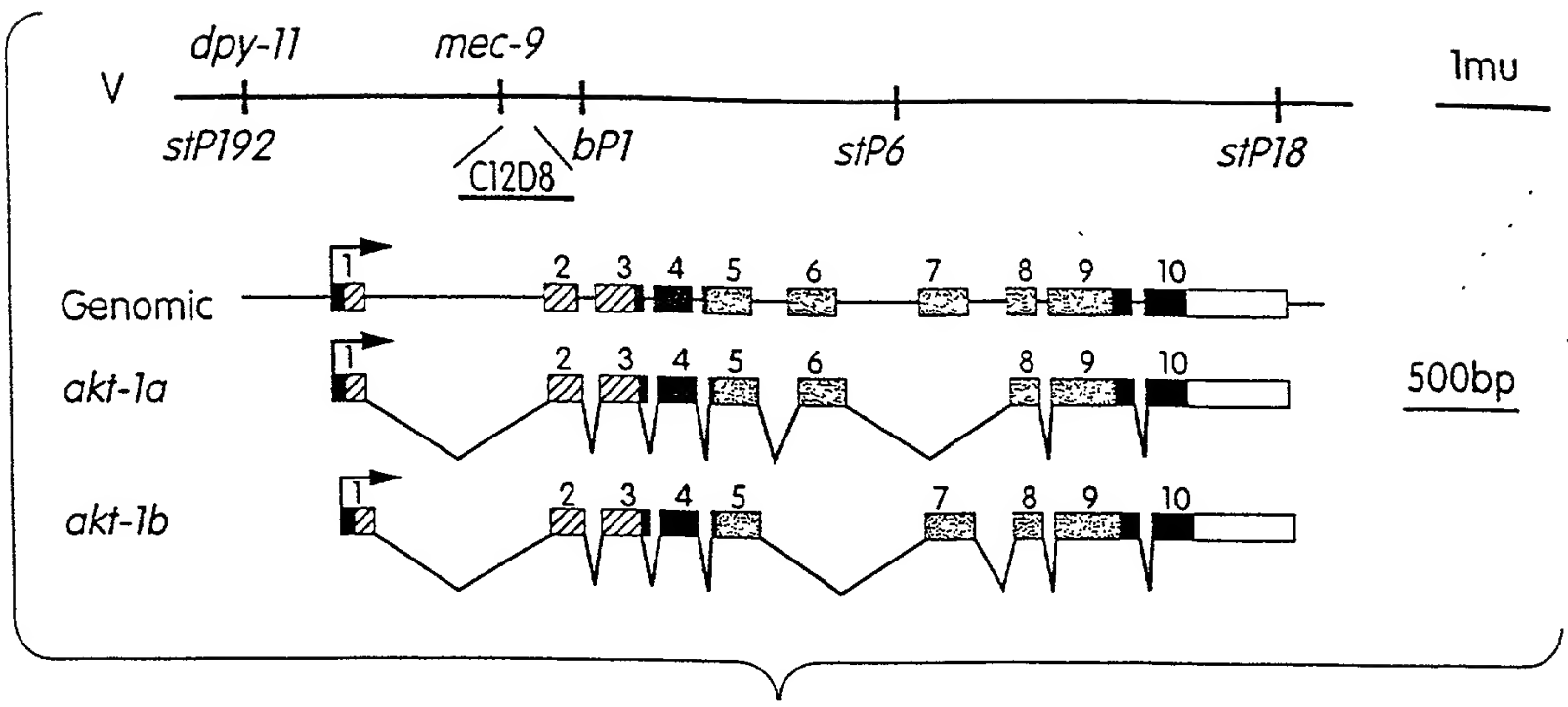
Zk84-6
Zk1251-2
C06e2
Zk75-3
Zk75-2
Ins-Human
Ins-Rabbit
Ins1-Xenopus
Ins2-Xenopus
Ins-Alligator
Ins-Elephantfish
Igf1-Bovine
Igf1-Dog
Igf2-Horse
Igf2-Human
Ilp-Amphioxus
Lirp-Locust
Bxa4-Bommo
Bxb1-Bommo
Bxrpa-Hornworm
Bxa1-Silkworm
Bxa2-Silkworm
Bxa3-Silkworm
F13b12
Mpi3-Seasnail
Relaxin-Human
Rlf-Human

Fig. 30


V
dpy-11
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1mu
stP192
C12D8
bP1
stP6
stP18
Genomic
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akt-1b
1
2
3
4
5
6
7
8
9
10
500bp

Fig. 31

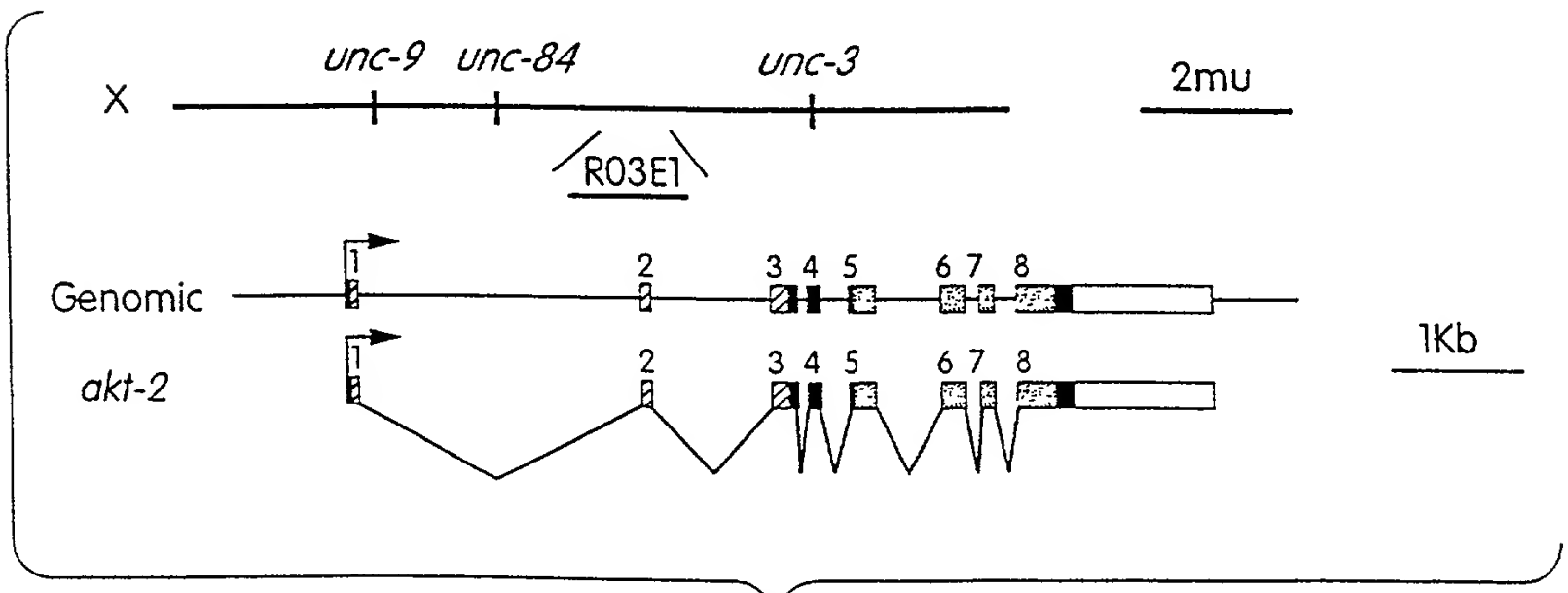
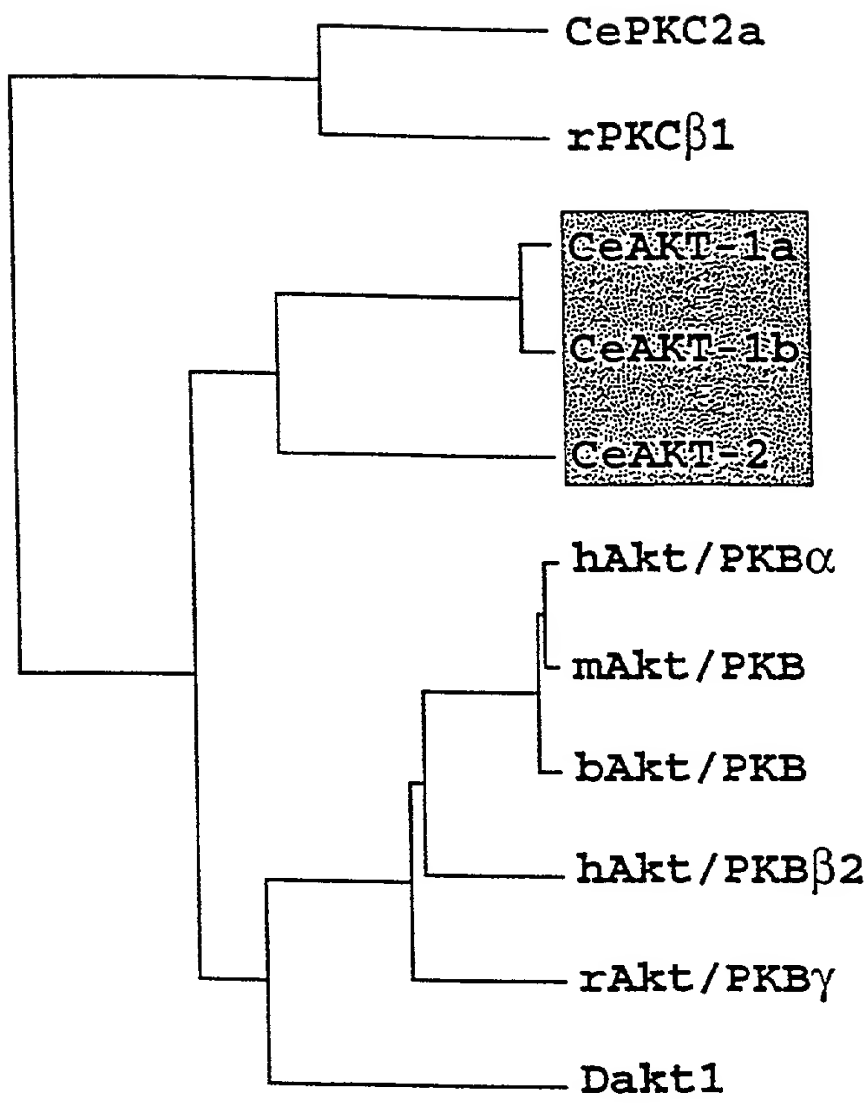

X
unc-9
unc-84
unc-3
2mu
R03E1
Genomic
akt-2
1
2
3
4
5
6
7
8
1Kb

Fig. 32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rPKCβ1
CeAKT-1a
CeAKT-1b
CeAKT-2
hAkt/PKBα
mAkt/PKB
bAkt/PKB
hAkt/PKBβ2
rAkt/PKBγ
Dakt1

Fig. 33

```
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AKT-1b      ............--...............................................................
AKT-2            M..ENAHLQK..I..S.....................IL.R..T.....S....D..L.....
hAkt/PKBa              MSDVAI.K.....R..Y.KT.....LLK...TFI.YKER.QDVDQREA..

AKT-1a      NDFMIKDAATMLFEKPRPNMFMVRCLQWTTVIERTFYAESAEVRQRWIHAIESIS--KKYKGTN
AKT-1b      ...........................................................--.........
AKT-2       .N...R...VCLD.....I.....................D..DF.....E..QAV.SHNRL.ENA
hAkt/PKBa   .N.SVAQCQL.KT.R....T.II.................HV.TP.E.EE.TT..QTVADGL.KQE--
                                                                    mg144 T
AKT-1a      ANPQEELMETNQQPKIDEDSEFAGAAHAIMGQPSSGHGDNCSIDFRASMISIADTSEAAKRDKI
AKT-1b      ............................................................
AKT-2       G.TSMQEED..GN.SGES.VNM---------DAT.TRS..---..ESTVMN.DEPE.VPRKNTV
hAkt/PKBa   ----------------E.EMD.----------R.GSPS..SGAE-------EMEV.L.KPKHRV

AKT-1a      TMEDFDFLKVLGKGTFGKVILCKEKRTQKLYAIKILKKDVIIAREEVAHTLTENRVLQRCKHPF
AKT-1b      ............................................................-.......
AKT-2       ..D.....Q.....R..SSD.....IR.EMVVD.S.....YA.V...
hAkt/PKBa   ..NE.EY..L.....V...A.GRY..M...E..V.KD.....NSR...

AKT-1a      LTELKYSFQEQHYLCFVMQFANGGELFTHVRK----CGTFSEPRARFYGAEIVLALGYLH-RC
AKT-1b      .....TNDR....E..I..D.YY.LNREVQMNKEG.....S.....-AN
AKT-2       .L.....A.YHL...E.....LQR-----K...A.T...S..I.....-HR
hAkt/PKBa   ..A.....THDR....EY.....F.LSRE-----RV..D.....S..D...SEK

AKT-1a      DIVYRDMKLENLLLDKDGHIKIADFGLCKEEISFGDKTSTFCGTPEYLAPEVLDDHDYGRCVDW
AKT-1b      S.....L.....................................................
AKT-2       N.....R.....T.....KY.....IE.I..D.S..
hAkt/PKBa   NV....L....M.....T.....G.KD.ATMK.....E.N...A...

AKT-1a      WGVGVVMYEMMCGRLPFYSKDHNKLFELIMAGDLRFPSKLSQEARTLLTGLLVKDPTQRLGGGP
AKT-1b      ............................................................
AKT-2       ..............SA.ENG.....TTC..K..NR..P..V...S...ERV.AK...A...
hAkt/PKBa   ..L..............NQ..E.....LMEEI...RT.GP..KS..S...K...K.....S

AKT-1a      EDALEICRADFERTVDWEATYRKEIEPPYKPNVQSETDTSYFDN-EFTSQPVQLTPPSRSGALA
AKT-1b      ..........................................-.................
AKT-2       D..R.VS..E..KD......L...V...F....M......F..RVRYV.ILLKV-----.E.I
hAkt/PKBa   ...K..MQHR..AGIV.QHV.E.KLS..F..Q.T.....R...E-...A.MITI...DQDDSME

AKT-1a      TVDEQEEMQSNFTQFSFHNVMGSINRIHEASEDNEDYDMGZ
AKT-1b      ..........................................
AKT-2
hAkt/PKBa   C..--S.RRPH.P...YSASSTA
```

Fig. 34

cataaaaatccagtaaatggtaaaattttcaatttcagatccatctcgatggaggatctcacaccaactaacacgtcgctcgacaccacaactac
taacaatgacacgacatcggatcgtgaagcggcgccaacggtgaggaactagtttctagacgaacatcggaatgcggcttaaagttcgggtgcac
ttatcaaactagacccgtttttagaccctctttcaaagcggggaactgcaatacacttttgaacctaaaacctagatttttggtgttctaaat
tcttttgtgaattggagagccaattcaaccggaaaactctttttttatagggaaaacgttttgccacgtagcagataagttaaatagaaaatattt
taaaatatttttttttgtctaggaaaaattgataaagcacctggtccaattttcagaacgttccaattttacctacaatacaaaattggccggca
agcttatggcttctgtttgcctacttctagcttgaacattctaaggctccgtagcgaaaaaatttttttaggctttttttaaataaatgtttggg
ccggaacacttaaccgaatagcatgatgaaacgctctaaaacttgaatttgaaaatttgcagttgatgctttaatataaaagttttgaggtttca
cctgcctaagatcgttttagcataaatatgtagatgaccgagagtatacaattaaatattaattaaatatgaatttcgaaatatgaattttggtt
gacttccattatgtttttttttttcacattttacaactattctaggcaaaaatgaaaaaaaaaacttgtagaataattttcaaaattttatttttc
cagacgctcaacttaacaccaacagcaagtgaatcggagaacagcttatccccagtcaccgccgaagatctcatagctaaaagcattaaagaagg
atgtccgaagagaacttccaacgacttcatgtttcttcagagtatgggcgaaggagcctacagccaggttggtgaacgaggaaatttccagaaat
gtgtgcaactagtatcagagtacaaggaaaagcttggaaaatactcggaatgcctgaattagtgcttgaagtaagcttgcccatttttttcggaa
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atatacctcactattagttaaatgctgagttttatcgattttatagctttttttacttatgtatattcaaaatgtatgtgtttttcaaatctt
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aaattggtttatttttttctagtccttgaattttcaccttcccatttttatgctctaactgtgtttcaaatactcatattccaacattgtaggaa
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ccactgaccgtaacacttttccaatggcgtatacaatttgaatttagcaacaaaacaaaaaaaaacaaaaatcgtaccaagacggactactgtat
ttttttggcggaaaaatcggccaatttttgcgtcagggttacacgactgtgggaattgaactcgcactatgtaggcccattcatgttgtctccccct
gtccaatctcttttctccacaacactttaatctcatttcgcatggagaagagaaagaagaagatgcagaaaacgacgacatcgtcatagaattgt
ctacacaaacctagtgttctgcgtctcttacacaaaataagccacgcgtctagcactatcaacattcgcaaacagctatacatgtgcttgttgaa
gggaaaaacgagacgtttgtgtgtattggggaggggtaatgtaaccgtggttgttgggttcatcaaattgacagcgcacagggatttgattttga
acgtgttatcgctttggaccctgaggcatgtttcctacacctagaacaactaccgtaatgaatctttacattgactttcggagagaagggtttgt
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gccccccccccctatacatatgatgcacacttaaaatgtccaagtggtgtttgaatagcaaatcttgaaaacgtaaaaacaataattatttttcta
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atattttctgcctcatattaaaaaatattcctctagcaaaaactgtaagttgaacgaatttacaataaaaaacacagctgcactgaccaaaaaac
aattacactggccaaaattgagcttgcactgaccgagtttagcgaccatatctttttgtctaatttgtggtgtgtgcggcgaattcggcaaaat
tgtcgagctcggaaaacagaaaatttggcaaatttaccgcaaactcttcaactgaagccactattgcacattaactgtcaaaattctggatataa
ttagcaaaacaataagtaacatttctgaaaaattagaacctttcccgcattgtatttgtagacgcacctaaaaaatttcaaaacaccaaaaaaca
agcttccagtaaaaccctaatattccaggtattccgatgtcgcgaagtggcaacagatgcgatgttcgccgtcaaagtgctccagaagtcgtacc
tcaaccgccatcaaaaaatggacgcaatcattcgcgagaagaatatcttaacatacctgtcacaagaatgcggtggtcatccgtttgtcacacag
ctctacacacattttcacgaccaggctagaatttgtgagtttttccagcgccaaggttcttttctgaacccatcaaaatccacttgtgatcatt
ttattccaataaaaacgtcaacttaaaaaaaaaattaaacctcaattaatattcagatttcgtgatcggacttgttgaaaatggtgatcttggcg
agtcgctgtgccattttggatcattcgacatgctcacctcaaaattctttgcctcggaaatcctcaccggactgcaattcctacacgacaacaaa
attgtgcacagagacatgaagccggacaatgtgctcatccagaaagacggtcacattctcatcacagattttggaagtgcccaggcgtttggcgg
tctccaactgtcacaggagggctttacggatgcgaatcaggcaagctcgcgatcttcggattctggatcgccgccgccaactcgattctattcgg
atgaggagggtaaggttttcggaaatttgactgaaacaatttttgccagttccagaagagaacactgctcgacgtaccacatttgttggaactgc
tctctacgtgagcccggagatgctagctgacggagatgtgggaccacagtaagctccgattctttgtagaatgtcaaatttaacagttggatttc
agaaccgacatttggggattgggatgtatccttttccagtgtctagccggacagccaccattcagagccgtcaaccagtaccatcttttgaaaag
aatccaggagttggatttctcgttcccagaaggatttccagaggaagcgtcggaaattatcgcaaag

Fig. 35A

attttggtaggttgacatgaaactttaaaaactgaatacgtaattttcaacttacaggtgcgcgacccgagtacccgtatcaccagtcaagaact
tatggctcacaagtttttgaaaacgttgactgggtgaacattgcaaatatcaagccaccagtcctgcacgcctacattccagccacatttggcg
agccggagtactactctaacattgggcctgtcgagccgggacttgatgatcGTGCCTTGTTCCGTTTGATGAATTTGGGAAATGATGCTAGCGCA
TCACAGCCATCAACGTGAGTTTGAAGCATTTTTTTCTTGCATTAAAAGTTTTACCTTGCACTGACCAAAATTTATTGAAACTATTAATTATTTGA
TTCTGATTAACAATGACCAAAAGATTTGAACTGACAAAGTGCAAATTTGCACCGACCAAAAAACAGTTTGCACTGACCACCTCTTCATTTGCACT
GACCACCTCTTCATTTGCACTGACCAACTTTTCATTTGCACTGACCATCTCTTCATTTGCACTGACCAACTTTTCATTTGCAATTCTGGCAATGA
TTCTTTTGCATCTACTGATCAAAAATTGATTCAAATCAATTAATTTTCTTTGACAGTACTATGCCTTATTCAAGGAGATGCTGATCTGAAAATTC
TCAATAGTTGATAAAAATTACTAACCCCTTAGAAAGTTTCAGACCGTCTAACGTGGAACATCGCGGAGACCCATTTGTTTCGGAAATTGCACCGT
GAGTGATTTGCACCTAATTGGTTATTTTTAATAATCATTAAATTATAGACGCGCCAATTCGGAAGCCGAAAAGAACCGCGCCGCACGTGCGCAGA
AGCTCGAAGAGCAACGTGTCAAAAACCCATTCCACATCTTCACCAACAACTCGCTCATTTTGAAACAAGGATATTTGGAAAAGAAGCGAGGATTG
TTTGCCAGACGCCGAATGTTCCTGTTGACCGAAGGACCGCATCTCTTGTACATTGATGTGCCGAATCTTGTGCTCAAAGGAGAGGTACCATGGAC
GCCGTGCATGCAGGTGGAGCTAAAAAACTCGGGAACTTTCTTTATACATACGGTAGGTCAGAATAATCATAGCTGTCTATCTCATTATAGTACTC
AATGAATCTGAAAATTTCAAATTTTCAGCCCAACCGCGTCTACTACTTGTTTGATCTCGAAAAGAAAGCAGATGAGTGGTGTAAGGCTATCAATG
ATGTTCGCAAGCGGTACTCGGTGACTATCGAAAAGACTTTTAACTCTGCGATGCGTGACGGAACATTTGGCAGCATTTATGGAAAGAAAAAGTCC
AGAAAGGTATGAATTACTGGAAGGCCCCCCTCACTGAGTTTCCAGCAAGTTCAGAGTTTTTTATTGGAATTTTTGCCAATTTTCATTAGACTTTA
GAGCCTATTGCTATTTTGTGGACAGGTTTAAACATTTTCAAAAAAAAATTGAGAAATGTCTGAAAAAATTTGGAGTGTGACAGTTTTCTGAATTT
TGAAAATTCTGTTCTCAAAATTGGATTTTTACAGAGCTTGTTTCGAGATTTCATAATCCTTCAAAAGAATATAGAATATTTGTGTTCAACTTTTC
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TCTTTATTTTCCATGCAACTCTAAAATCTTCCCGTATATTTTTTTGGAAAGTCTTATGATGTTTAGACGGTTTAAATTTTTTGATGATTTAAATT
TTTTAGGGGTGGTCTATAATTTTGGACCACCCTGTATAATTATGGACCACCATGTACACTTATAGACCACCCAGTAACAAGCATTTTTGGACCAC
CACGCAAATCTTATTATTATGGACCACCCAAACTTAGAACACCTTCAATACTTCTTTTCTGTTCAAAAAATGATCAACTTGCTGAAAAAAAATTT
TTTGTAGGAAATGATGCGTGAACAGAAGGCGCTGCGCCGCAAACAAGAAAAGGAGGAGAAAAAGGCGCTAAAAGCCGAGCAAGTGAGCAAGAAGC
TTTCAATGCAAATGGACAAGAAGTCGCCTTGAAGGCTCACCTCCCTTCTACTCCCCACAAAATCACCATCAAACAAATCACACTTTTGTATCATT
TTGCGTCC

Fig. 35B

MEDLTPTNTSLDTTTTNNDTTSDREAAPTTLNLTPTASESENSLSPVTAEDLIAKSIKEGCPKRTSNDFMFLQSMGEG
AYSQVFRCREVATDAMFAVKVLQKSYLNRHQKMDAIIREKNILTYLSQECGGHPFVTQLYTHFHDQARIYFVIGLV
ENGDLGESLCHFGSFDMLTSKFFASEILTGLQFLHDNKIVHRDMKPDNVLIQKDGHILITDFGSAQAFGGLQLSQEGFT
DANQASSRSSDSGSPPPTRFYSDEEEENTARRTTFVGTALYVSPEMLADGDVGPQTDIWGLGCILFQCLAGQPPFRAV
NQYHLLKRIQELDFSFPEGFPEEASEIIAKILVRDPSTRITSQELMAHKFFENVDWVNIANIKPPVLHAYIPATFGEP
EYYSNIGPVEPGLDDRALFRLMNLGNDASASQPSTPSNVEHRGDPFVSEIAPRANSEAEKNRAARAQKLEEQRVK
NPFHIFTNNSLILKQGYLEKKRGLFARRRMFLLTEGPHLLYIDVPNLVLKGEVPWTPCMQVELKNSGTFFIHTPNR
VYYLFDLEKKADEWCKAINDVRKRYSVTIEKTFNSAMRDGTFGSIYGKKKSRKEMMREQKALRRKQEKEEKKAL
KAEQVSKKLSMQMDKKSP

Fig. 36

MEDLTPTNTSLDTTTTNNDTTSDREAAPTTLNLTPTASESENSLSPVTAEDLIAKSIKEGCPKRTSNDFMFLQSMGEG
AYSQVFRCREVATDAMFAVKVLQKSYLNRHQKMDAIIREKNILTYLSQECGGHPFVTQLYTHFHDQARIYFVIGLV
ENGDLGESLCHFGSFDMLTSKFFASEILTGLQFLHDNKIVHRDMKPDNVLIQKDGHILITDFGSAQAFGGLQLSQEGFT
DANQASSRSSDSGSPPPTRFYSDEEVPEENTARRTTFVGTALYVSPEMLADGDVGPQTDIWGLGCILFQCLAGQPPFR
AVNQYHLLKRIQELDFSFPEGFPEEASEIIAKILVRDPSTRITSQELMAHKFFENVDWVNIANIKPPVLHAYIPATF
GEPEYYSNIGPVEPGLDDRALFRLMNLGNDASASQPSTFRPSNVEHRGDPFVSEIAPRANSEAEKNRAARAQKLEE
QRVKNPFHIFTNNSLILKQGYLEKKRGLFARRRMFLLTEGPHLLYIDVPNLVLKGEVPWTPCMQVELKNSGTFFIH
TPNRVYYLFDLEKKADEWCKAINDVRKRYSVTIEKTFNSAMRDGTFGSIYGKKKSRKEMMREQKALRRKQEKEE
KKALKAEQVSKKLSMQMDKKSP

Fig. 37

TD5260"E59E9650

FIG. 38A

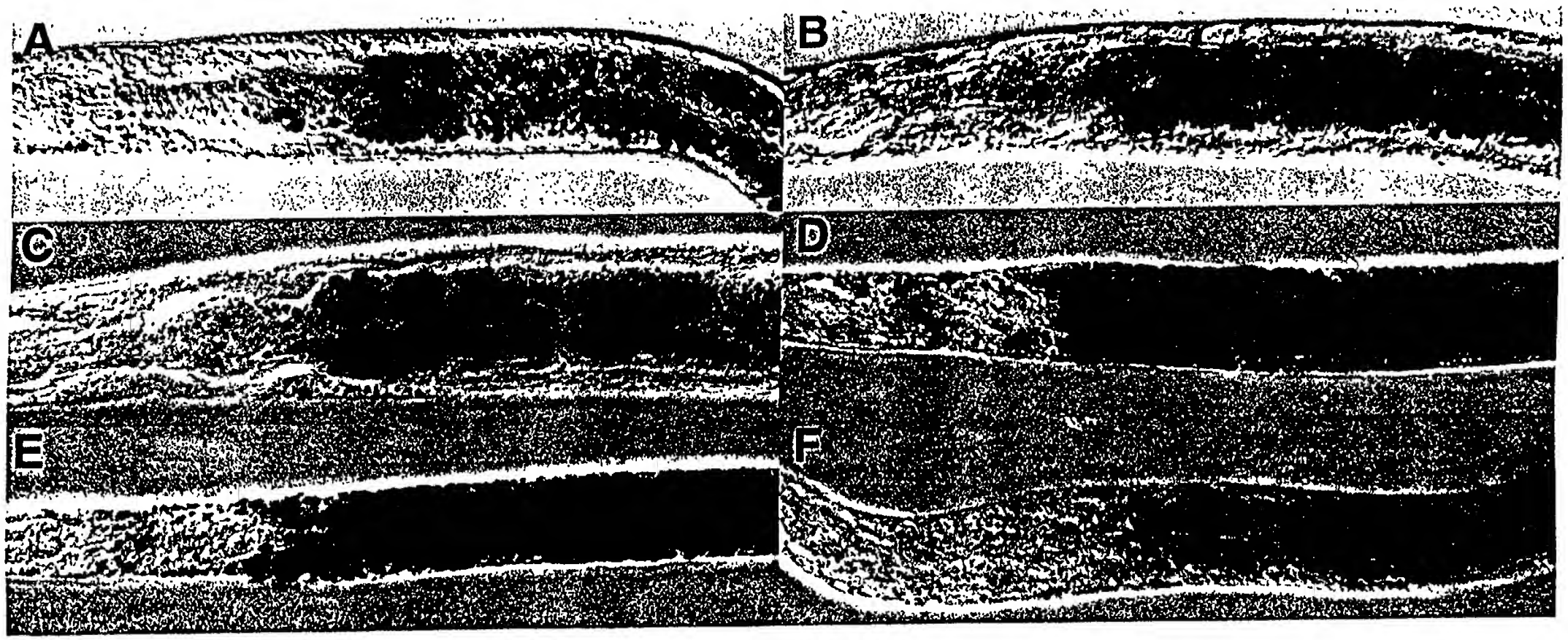


FIG. 38B

FIG. 38C

FIG. 38D

FIG. 38E

FIG. 38F

FIG. 39A

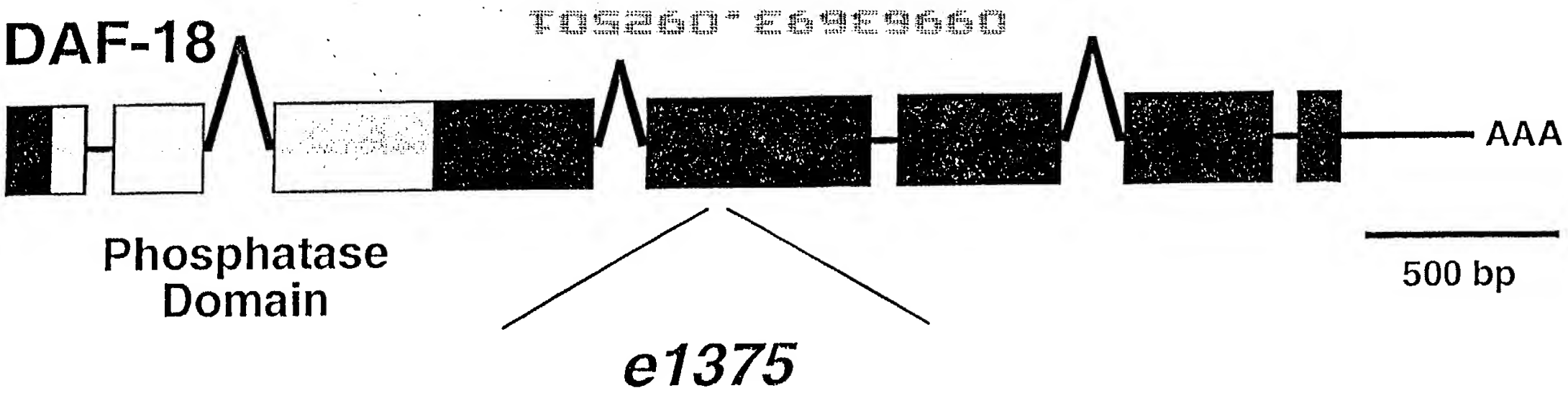


FIG. 39B

```
DAF-18   48 IFRTAVSSNR CRTEYQNIDL DCAYITDRLI AIGYPATGIE ANFRNSKVQT
PTEN      4 TIKEIVSRNK RRYQEDGFDL DLTYIYPNII AMGFPAERLE GVYRNNIDDV

DAF-18   98 QQFLTRRHGK GNVKVFNLRG GYYVDADNFD GNVICFDMTD HHPPSLELMA
PTEN     54 VRELDSKHRK NHYKIYNLCA ERHYDTAKFN CRVAQYPFED HNPPQLELIK

DAF-18  148 PFCREAKEWL EADDKHVIAV HCKAGKGRTG VMICALLIYI NFYPSPRQIL
PTEN    103 PFCEDLDQWL SEDDNHVAAI HCKAGKGRTG VMICAYLLHR GKFLKAQEAL

DAF-18  198 DYYSIIRTKN NKGVTIPSQR RYIYYYHKLR ERELNYLPLR MQLIGVYVER
PTEN    153 DFYGEVRTRD KKGVTIPSQR RYVYYYSYLL KNHLDYRPVA LLFHKMMFET

DAF-18  248 PPKTWGGGSK IKVEVGNGST ILFKPD..PL IISKSNHQRE RATWLNNCDT
PTEN    203 IPMFSGGTCN PQFVVCQLKV KIYSSNSGPT RREDKFMYFE FPQPLPVCGD
```

DAF-18 Protein

MVTPPPDVPSTSTRSMARDLQENPNRQPGEPRVSEPYHNSIVERIRHIFRTAVSSNRCRTEYQNIDLDCAYITDRIIAIG
YPATGIEANFRNSKVQTQQFLTRRHGKGNVKVFNLRGGYYYDADNFDGNVICFDMTDHHPPSLELMAPFCREAKEWLEAD
DKHVIAVHCKAGKGRTGVMICALLIYINFYPSPRQILDYYSIIRTKNNKGVTIPSQRRYIYYYHKLRERELNYLPLRMQL
IGVYVERPPKTWGGGSKIKVEVGNGSTILFKPDPLIISKSNHQRERATWLNNCDTPNEFDTGEQKYHGFVSKRAYCFMVP
EDAPVFVEGDVRIDIREIGFLKKFSDGKIGHVWFNTMFACDGGLNGGHFEYVDKTQPYIGDDTSIGRKNGMRRNETPMRK
IDPETGNEFESPWQIVNPPGLEKHITEEQAMENYTNYGMIPPRYTISKILHEKHEKGIVKDDYNDRKLPMGDKSYTESGK
SGDIRGVGGPFEIPYKAEEHVLTFPVYEMDRALKSKDLNNGMKLHVVLRCVDTRDSKMMEKSEVFGNLAFHNESTRRLQA
LTQMNPKWRPEPCAFGSKGAEMHYPPSVRYSSNDGKYNGACSENLVSDFFEHRNIAVLNRYCRYFYKQRSTSRSRYPRKF
RYCPLIKKHFYIPADTDDVDENGQPFFHSPEHYIKEQEKIDAEKAAKGIENTGPSTSGSSAPGTIKKTEASQSDKVKPAT
EDELPPARLPDNVRRFPVVGVDFENPEEESCEHKTVESIAGFEPLEHLFHESYHPNTAGNMLRQDYHTDSEVKIAEQEAK
AFVDQLLNGQGVLQEFMKQFKVPSDNSFADYVTGQAEVFKAQIALLEQSEDFQRVQANAEEVDLEHTLGEAFERFGHVVE
ESNGSSKNPKALKTREQMVKETGKDTQKTRNHVLLHLEANHRVQIERRETCPELHPEDKIPRIAHFSENSFSDSNFDQAI
YL

FIG. 40A

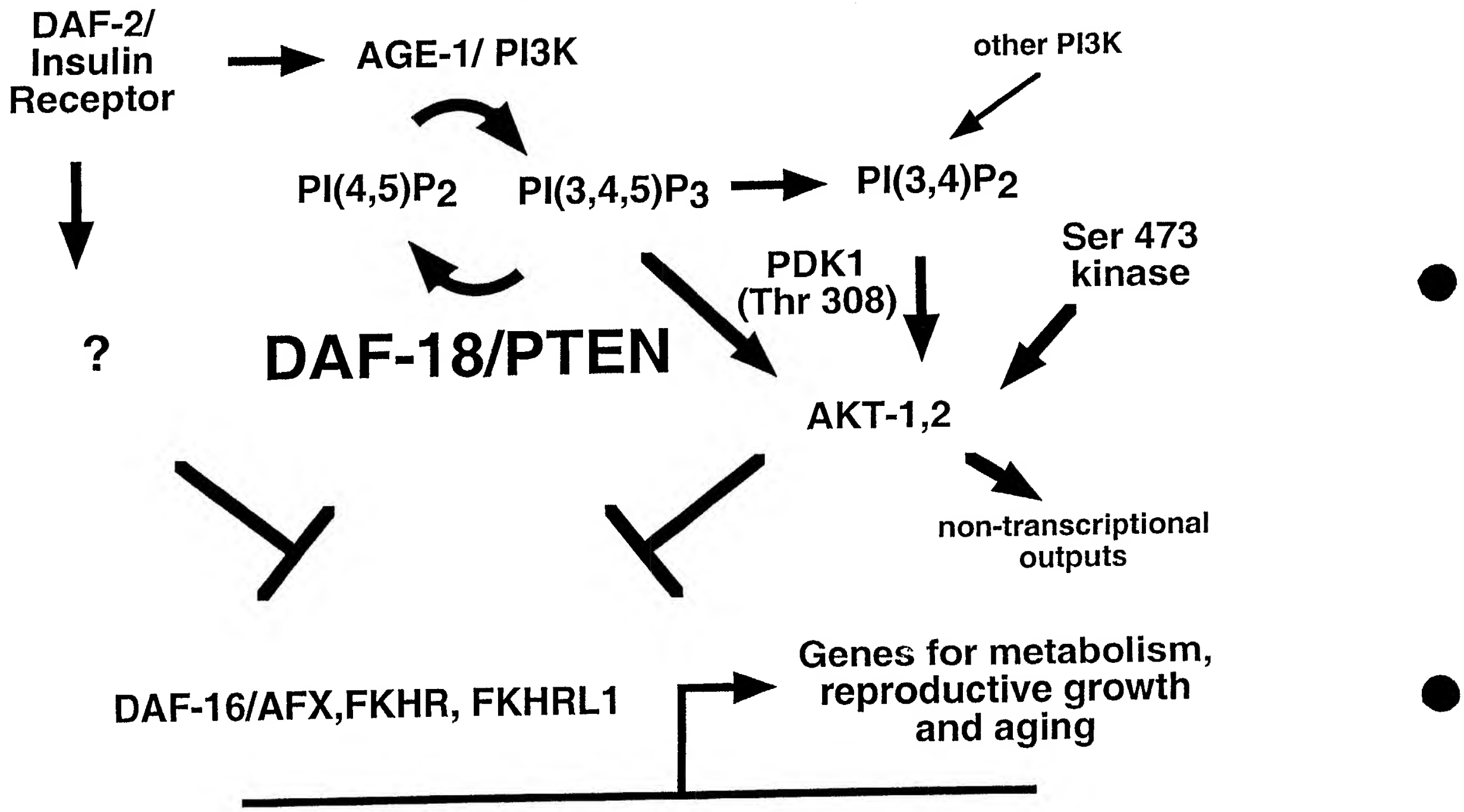
```
   1 ttccaggtac atctactaac ccccaatggt tactcctcct ccagatgtgc caagcacatc
  61 gaccaggtcg atggctcgtg accttcaaga gaatccaaac cgacaacctg gtgaaccacg
 121 tgtgtctgaa ccgtatcaca attcaatcgt cgagcggatt cgccatattt ttcggacggc
 181 tgtatcttcc aatcgttgtc gcaccgagta ccaaaatatc gacctagatt gtgcatatat
 241 cacagaccga atcatagcta tcggttatcc agcaacagga atcgaagcga atttccgtaa
 301 ctcaaaagtt caaactcaac aatttctgac caggcggcac ggaaagggca acgtgaaggt
 361 gtttaacctg cgcggtggat actactacga tgcggataac ttcgatggaa atgttatttg
 421 cttcgatatg actgatcatc atccgccgag tctcgaatta atggctccgt tttgcagaga
 481 ggctaaggaa tggcttgaag cagacgataa acatgtaata gctgtacact gtaaagctgg
 541 aaaaggccgt accggagtga tgatatgtgc tcttctcatc tacatcaact tctatccgag
 601 cccacgacaa attctcgact actactcaat aattcgtaca aaaaacaaca aaggtgtcac
 661 aattccatca caacgacgct acatttacta ctaccataag cttcgtgaac gtgagctcaa
 721 ctatttacca ttgagaatgc agttgattgg tgtctacgtg gaacggcctc caaagacatg
 781 gggtggtggt tcaaagataa aagtggaggt tggaaatggc tcgacaattt tatttaagcc
 841 ggatcctctc ataatctcca aatcaaatca tcagcgagag cgtgcgacgt ggctgaacaa
 901 ctgtgatacg cctaacgaat tcgacaccgg agagcaaaaa tatcatggat ttgtttccaa
 961 gagagcatac tgttttatgg tgccagaaga tgctccagta tttgtcgaag gagatgttcg
1021 tatagacatt cgcgaaatcg gatttctcaa aaagttttcg gacgggaaga ttggtcatgt
1081 ttggttcaat acaatgttcg catgtgatgg aggactcaac ggtggacatt tcgagtacgt
1141 agacaaaact cagccgtaca tcggagacga tacatcaatc ggacggaaaa atggaatgcg
1201 aagaaatgaa acgccgatgc gaaaaattga tccagaaact ggaaatgaat ttgagtctcc
1261 gtggcaaata gtgaatcctc ctggactgga aaaacatatt acggaggaac aagcaatgga
1321 aaattatacc aattatggca tgattcctcc tcgatacacg atcagcaaga ttcttcacga
1381 aaagcatgaa aaaggtatcg tcaaggatga ctataatgat cgtaagctgc caatgggaga
1441 caaatcatac acggaatcag gaaaaagtgg agatattcga ggagtcggtg gtccatttga
1501 gataccatat aaagctgagg aacatgttct cacatttcca gtttatgaaa tggatcgagc
1561 attgaagagt aaagatctta acaacggaat gaaacttcac gttgttcttc gttgtgtaga
1621 tactcgtgat tcaaaaatga tggaaaagag cgaagtgttc ggcaatctgg cattccataa
1681 tgaatcgaca cggaggcttc aagcgttgac tcaaatgaat ccaaaatggc gacctgaacc
1741 gtgtgcgttc ggatccaaag gtgctgaaat gcattaccct ccgtcggttc gatattcaag
1801 caatgatgga aagtataatg gagcctgcag tgagaacctt gttagcgatt ttttcgagca
1861 cagaaatatt gccgttctta atcgatattg ccgatatttc tacaagcaac gcagtacatc
1921 tcgaagccgt tatccaagaa aattcagata ctgtcctctg atcaagaaac atttctacat
1981 tccagctgat accgatgatg ttgatgaaaa tgggcaaccg ttcttccact caccagagca
2041 ttacattaaa gaacaggaaa aaatagacgc agagaaagca gctaaaggaa ttgaaaatac
2101 tggacccagt acttcaggat caagtgctcc cggaactatc aagaaaacgg aagcttcaca
2161 atccgacaag gtgaagccgg caactgaaga cgaacttcct cctgcgaggc taccggataa
2221 tgtgcgaaga tttccagtcg tcggcgttga tttcgaaaat ccggaagaag aatcgtgtga
2281 acacaaaacc gtagagtcaa tagctggttt tgaaccactc gaacatctat tccatgaatc
2341 ataccatcca aatacggccg gtaacatgct gcgtcaggat tatcacactg attcggaagt
2401 gaaaatagct gaacaagagg caaaagcctt cgttgaccag ttgcttaatg gacaaggtgt
2461 attacaagag tttatgaagc aattcaaagt accatcggac aattcctttg ctgattatgt
2521 aaccggacag gccgaagttt ttaaagcaca gattgcgtta ctggagcagt cggaggattt
2581 tcaacgagtt caagcgaatg cagaggaagt cgatcttgaa cacactcttg gtgaagcgtt
2641 tgagcgattc gggcacgttg tagaagaatc gaatggttct tctaaaaatc caaaagccct
2701 gaaaactcga gaacaaatgg tgaaagaaac tggcaaagac actcagaaga cccgcaatca
2761 tgtgcttcta catttggaag ctaatcatcg tgtgcaaatc gagcgtcgtg aaacgtgccc
```

FIG. 40B

2821 ggagctacat ccagaggata aaatcccaag aattgctcat ttttccgaaa acagcttctc
2881 ggattcgaat tttgatcaag ctatttattt gtaaacctaa aacaaaactt ttagaagatt
2941 ttcttcttac tgaccctcca attttcagat aatttcaatg ttttaagttt tctcttcaaa
3001 gtatcattca ctttctgtat agtgttttgt tttttaacaa actattgttc gattattttg
3061 tatattcata ttatagctct caacttcccg attttccacg tatatatgta tattttgccg
3121 ggtgaaaaat agcaattccc tatgaatgta tccccttcca tctgttttct tactcagaaa
3181 ttgtaattca cattgcgggt catcactaat cctatgggct ttaacacaat tctcccataa
3241 attaattgta cttaccaatt ttttgtttaa ttatttagat ttgtaacatt gaaattggtg
3301 ataa

FIG. 40B

FIG. 41


DAF-2/
Insulin
Receptor
AGE-1/ PI3K
other PI3K
PI(4,5)P2
PI(3,4,5)P3
PI(3,4)P2
PDK1
(Thr 308)
Ser 473
kinase
?
DAF-18/PTEN
AKT-1,2
non-transcriptional
outputs
DAF-16/AFX,FKHR, FKHRL1
Genes for metabolism,
reproductive growth
and aging

ttta

attacccaagtttgaggtagcattgctcttcaatcat atg gat tcg ttg ttt cag atg gca tcc gca
M D S L F Q M A S A

atg aag ttt caa tac tac tcg aag aaa gct gct gga aag aca atg tct aat agt gtc tcc
M K F Q Y Y S K K A A G K T M S N S V S

atg tcc agt gac aat cgc atg gag gat ttt aaa cgt cgt ttt cgt cga agt gga tcg tta
M S S D N R M E D F K R R F R R S G S L

gga att cca ttt gtc cca gaa gaa gat gtt aaa caa ctc ttc aca cca act cgt act gtt
G I P F V P E E D V K Q L F T P T R T V

cgt cga gaa gca tct att cgc gaa ggg gat gag gaa gaa gga gta caa att ctc aca ata
R R E A S I R E G D E E E G V Q I L T I

att gtc aag tca agt cgt gtt tcg gag gat atc tca aaa atg att gca aac ctc cct gat
I V K S S R V S E D I S K M I A N L P D

cac act cgt atc aaa cat ttg gag act cgt gac agt caa gat gga agt tcc aaa act atg
H T R I K H L E T R D S Q D G S S K T M

gat gtt ctt cta gag att gag ctc ttt cat tat gga aaa caa gaa gca atg gat ctt atg
D V L L E I E L F H Y G K Q E A M D L M

aga ctt aat ggg ctt gat gtt cat gag gtg tca tcg act att cgt cca act gca ata aaa
R L N G L D V H E V S S T I R P T A I K

gag caa tat aca gag cct gga tct gat gat gcg aca acc ggt tct gaa tgg ttt cca aaa
E Q Y T E P G S D D A T T G S E W F P K

agt att tat gat ttg gat att tgt gca aaa aga gtg att atg tat gga gca ggg ctg gac
S I Y D L D I C A K R V I M Y G A G L D

gct gat cat cct ggt ttc aaa gat acc gag tat cgt caa cgt cga atg atg ttt gct gaa
A D H P G F K D T E Y R Q R R M M F A E

ctg gcg ctc aat tac aaa cac ggt gag cca att ccg cga acc gaa tat aca tca tcc gaa
L A L N Y K H G E P I P R T E Y T S S E

cgg aaa act tgg gga att ata tat aga aaa ttg aga gaa ttg cac aaa aag cac gca tgc
R K T W G I I Y R K L R E L H K K H A C

aag cag ttt ctt gat aac ttt gag cta ctg gag aga cat tgt gga tac tcg gaa aat aat
K Q F L D N F E L L E R H C G Y S E N N

att ccg caa cta gaa gat atc tgc aag ttt ttg aaa gca aaa act gga ttc cgt gtt cgc
I P Q L E D I C K F L K A K T G F R V R

FIG. 42

```
cca gtc gcc gga tac tta tca gct cgt gat ttc ttg gca ggt ctt gca tat cgt gtc ttc
P   V   A   G   Y   L   S   A   R   D   F   L   A   G   L   A   Y   R   V   F

ttc tgc act caa tac gtt cgc cat cat gcc gat cca ttt tac act cca gaa cca gac acc
F   C   T   Q   Y   V   R   H   H   A   D   P   F   Y   T   P   E   P   D   T

gtt cac gag ctc atg ggt cac atg gct cta ttc gct gat cca gat ttt gct cag ttt tct
V   H   E   L   M   G   H   M   A   L   F   A   D   P   D   F   A   Q   F   S

caa gag att gga tta gct tct ctt gga gca tca gag gaa gat ttg aag aag ctt gca aca
Q   E   I   G   L   A   S   L   G   A   S   E   E   D   L   K   K   L   A   T

ctc tac ttc ttt tcc att gaa ttt ggt ctc tcg tct gat gac gct gcc gat tct cca gta
L   Y   F   F   S   I   E   F   G   L   S   S   D   D   A   A   D   S   P   V

aaa gaa aat gga tca aat cat gaa aga ttt aaa gta tac gga gca gga ctt ctg agc agt
K   E   N   G   S   N   H   E   R   F   K   V   Y   G   A   G   L   L   S   S

gct ggc gag ttg caa cat gcc gtt gag ggt agt gca acc att att cgt ttt gat ccg gat
A   G   E   L   Q   H   A   V   E   G   S   A   T   I   I   R   F   D   P   D

cgt gtt gtt gag caa gaa tgt ctc att act act ttc cag tca gcg tat ttc tat act aga
R   V   V   E   Q   E   C   L   I   T   T   F   Q   S   A   Y   F   Y   T   R

aat ttt gaa gag gcc cag cag aaa ctc aga atg ttc acc aac aac atg aaa cgt ccc ttc
N   F   E   E   A   Q   Q   K   L   R   M   F   T   N   N   M   K   R   P   F

att gtt cgt tac aac cca tac aca gaa agc gtc gaa gtt ctc aac aac tcc cgt tcc att
I   V   R   Y   N   P   Y   T   E   S   V   E   V   L   N   N   S   R   S   I

atg ttg gca gtg aac tct ctc cgc tca gac atc aac ctg ctc gcc gga gct ctc cac tac
M   L   A   V   N   S   L   R   S   D   I   N   L   L   A   G   A   L   H   Y

atc ctg tag
I   L   *
```

FIG. 42

attacccaagtttgaggtagcattgctcttcttcaatcat

atg gat tcg ttg ttt cag atg gca tcc gca atg aag ttt caa tac tac tcg aag aaa gct
M D S L F Q M A S A M K F Q Y Y S K K A

gct gga aag aca atg tct aat agt gtc aaa aac tgg att ccg tgt tcg ccc agt cgc cgg
A G K T M S N S V K N W I P C S P S R R

ata ctt atc agc tcg tga ttt ctt ggc agg tct tgc ata tcg tgt ctt ctt ctg cac tca
I L I S S *

ata cgt tcg cca tca tgc cga tcc att tta cac tcc aga acc aga cac cgt tca cga gct

cat ggg tca cat ggc tct att cgc tga tcc aga ttt tgc tca gtt ttc tca aga gat tgg

att agc ttc tct tgg agc atc aga gga aga ttt gaa gaa gct tgc aac act cta ctt ctt

ttc cat tga att tgg tct ctc gtc tga tga cgc tgc cga ttc tcc agt aaa aga aaa tgg

atc aaa tca tga aag att taa agt ata cgg agc agg act tct gag cag tgc tgg cga gtt

gca aca tgc cgt tga ggg tag tgc aac cat tat tcg ttt tga tcc gga tcg tgt tgt tga

gca aga atg tct cat tac tac ttt cca gtc agc gta ttt cta tac tag aaa ttt tga aga

ggc cca gca gaa act cag aat gtt cac caa caa cat gaa acg tcc ctt cat tgt tcg tta

caa ccc ata cac aga aag cgt cga agt tct caa caa ctc ccg ttc cat tat gtt ggc agt

gaa ctc tct ccg ctc aga cat caa cct gct cgc cgg agc tct cca cta cat cct gta g

FIG. 43

FIG. 44A

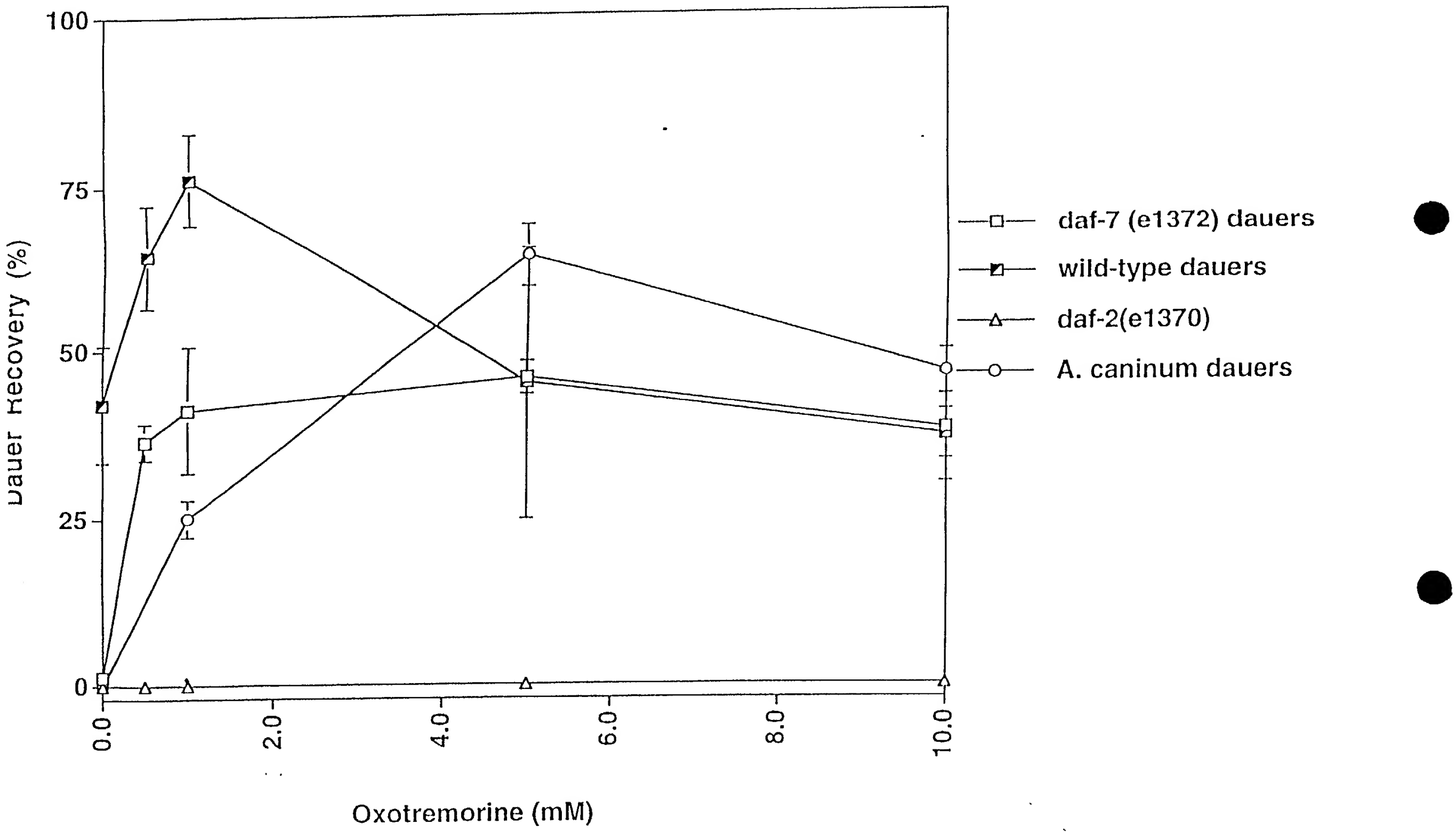

100
75
50
25
0
Dauer Recovery (%)
0.0
2.0
4.0
6.0
8.0
10.0
Oxotremorine (mM)
daf-7 (e1372) dauers
wild-type dauers
daf-2(e1370)
A. caninum dauers

FIG. 44B

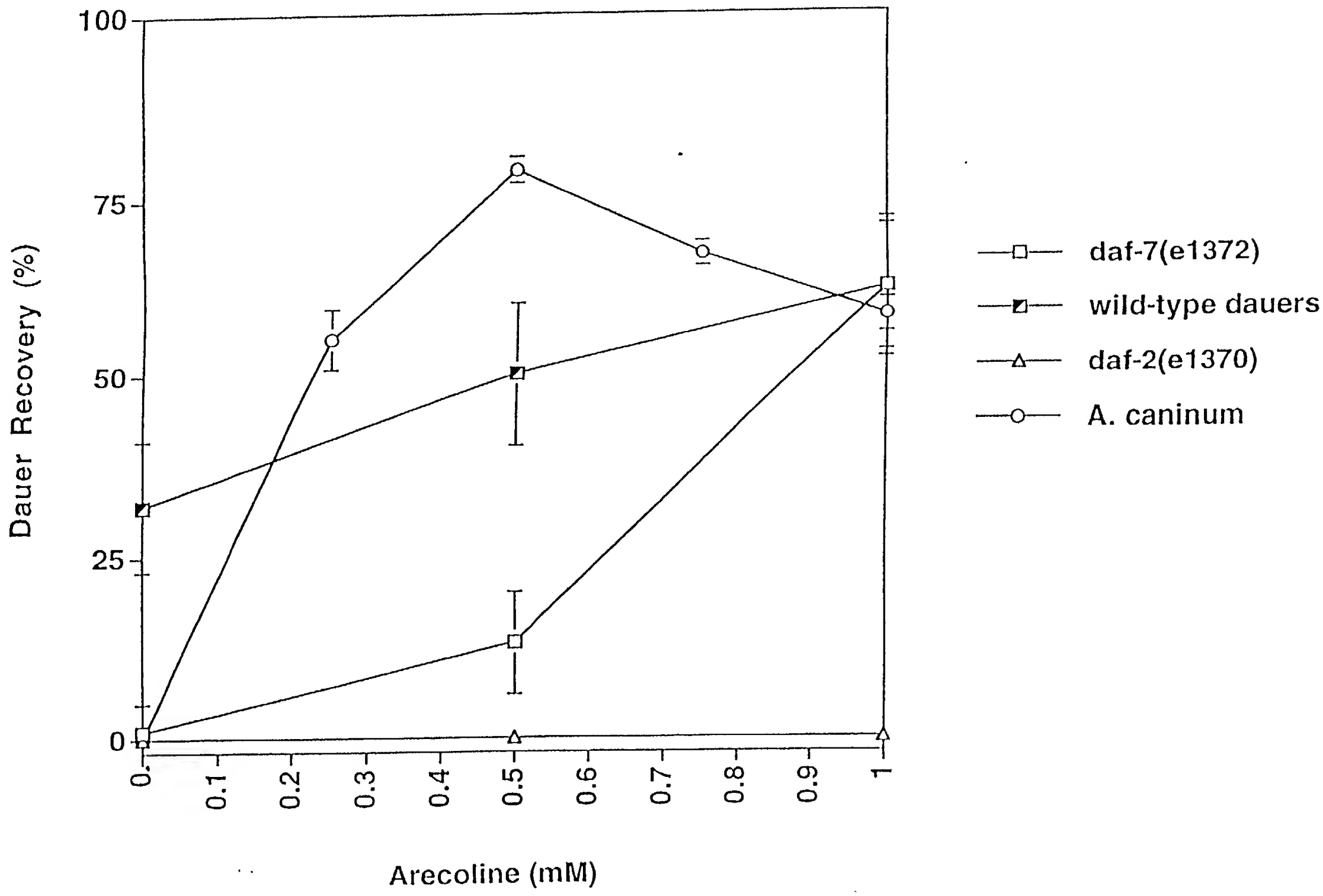

100
75
50
25
0
Dauer Recovery (%)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
Arecoline (mM)
daf-7(e1372)
wild-type dauers
daf-2(e1370)
A. caninum

FIG. 45A

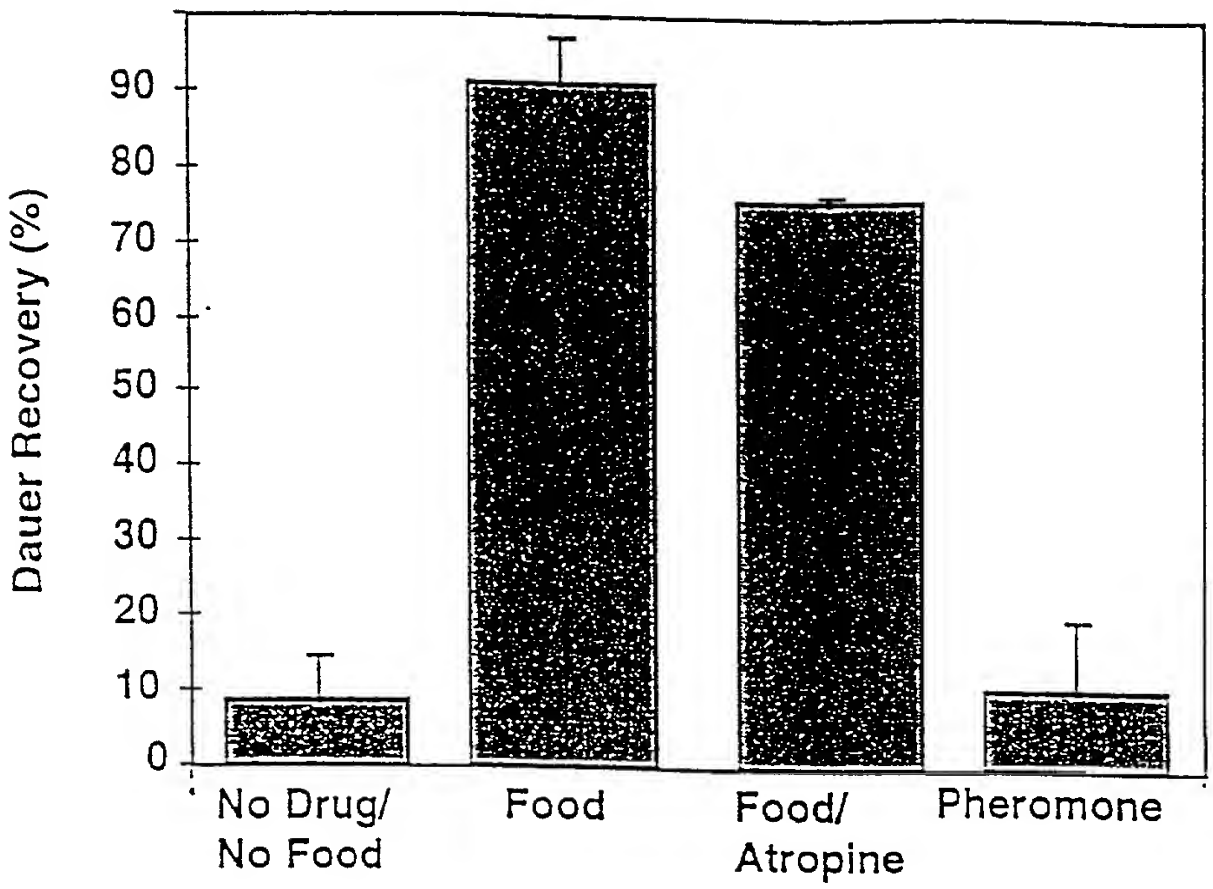

Dauer Recovery (%)
90
80
70
60
50
40
30
20
10
0
No Drug/ No Food
Food
Food/ Atropine
Pheromone

FIG. 45B

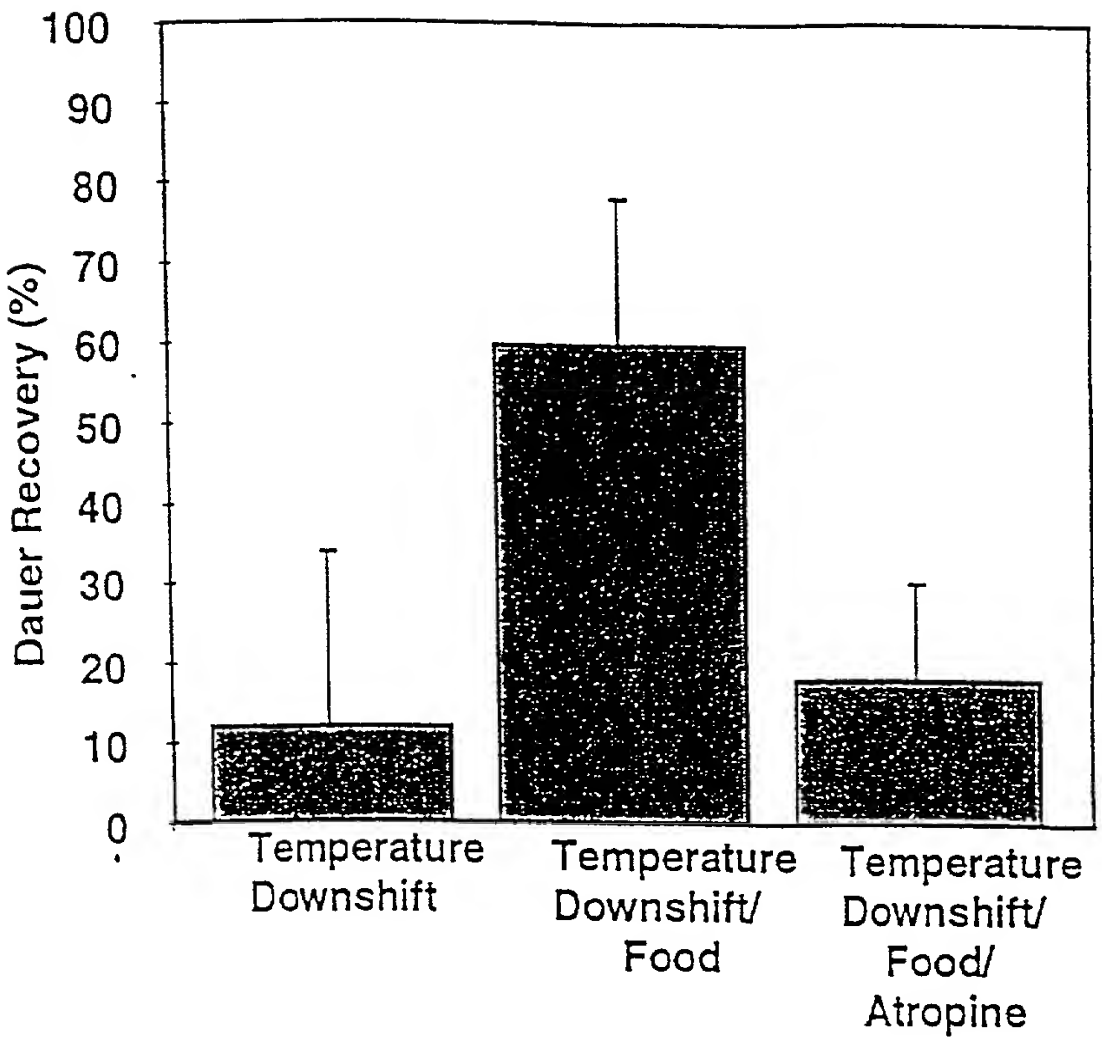
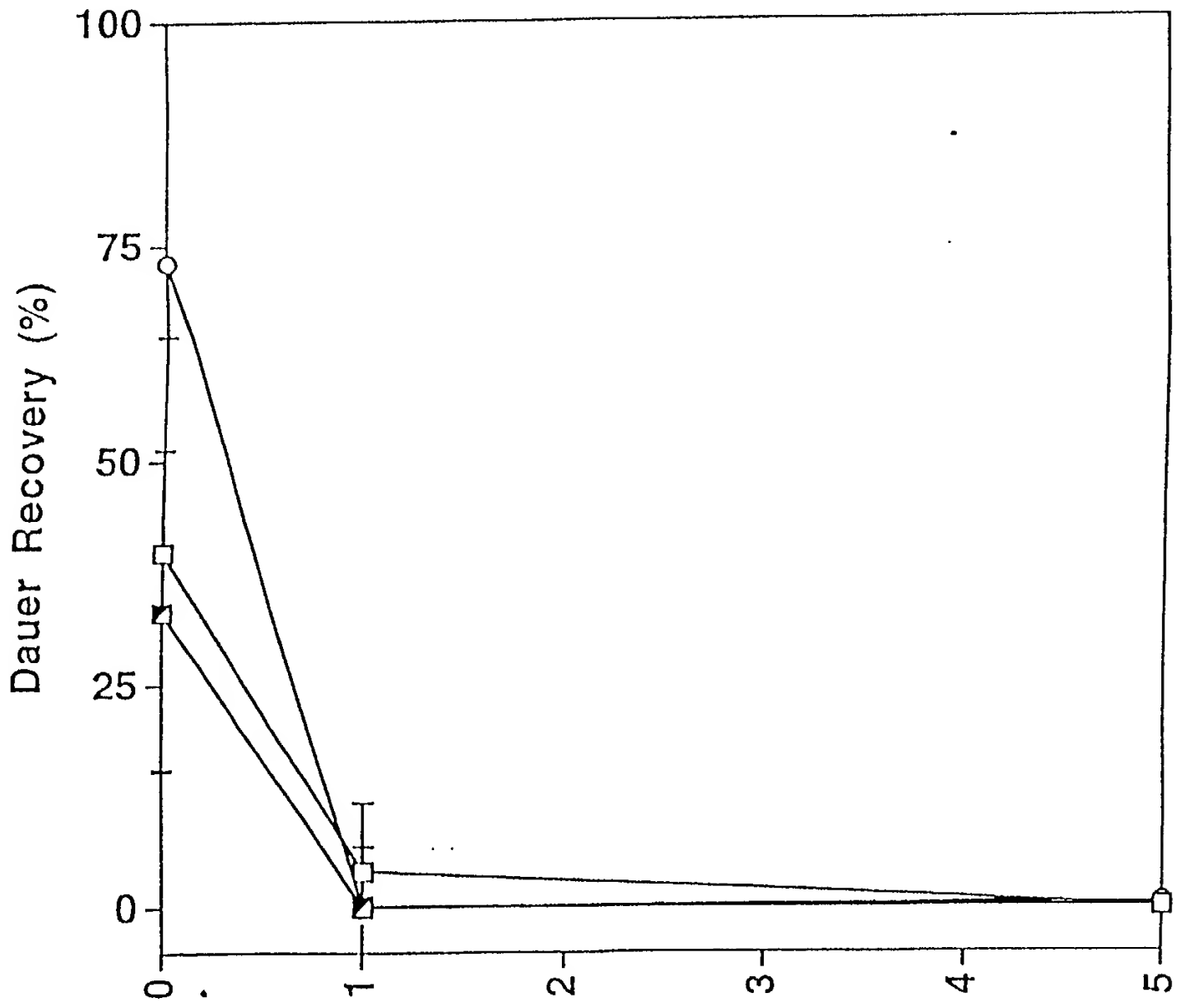
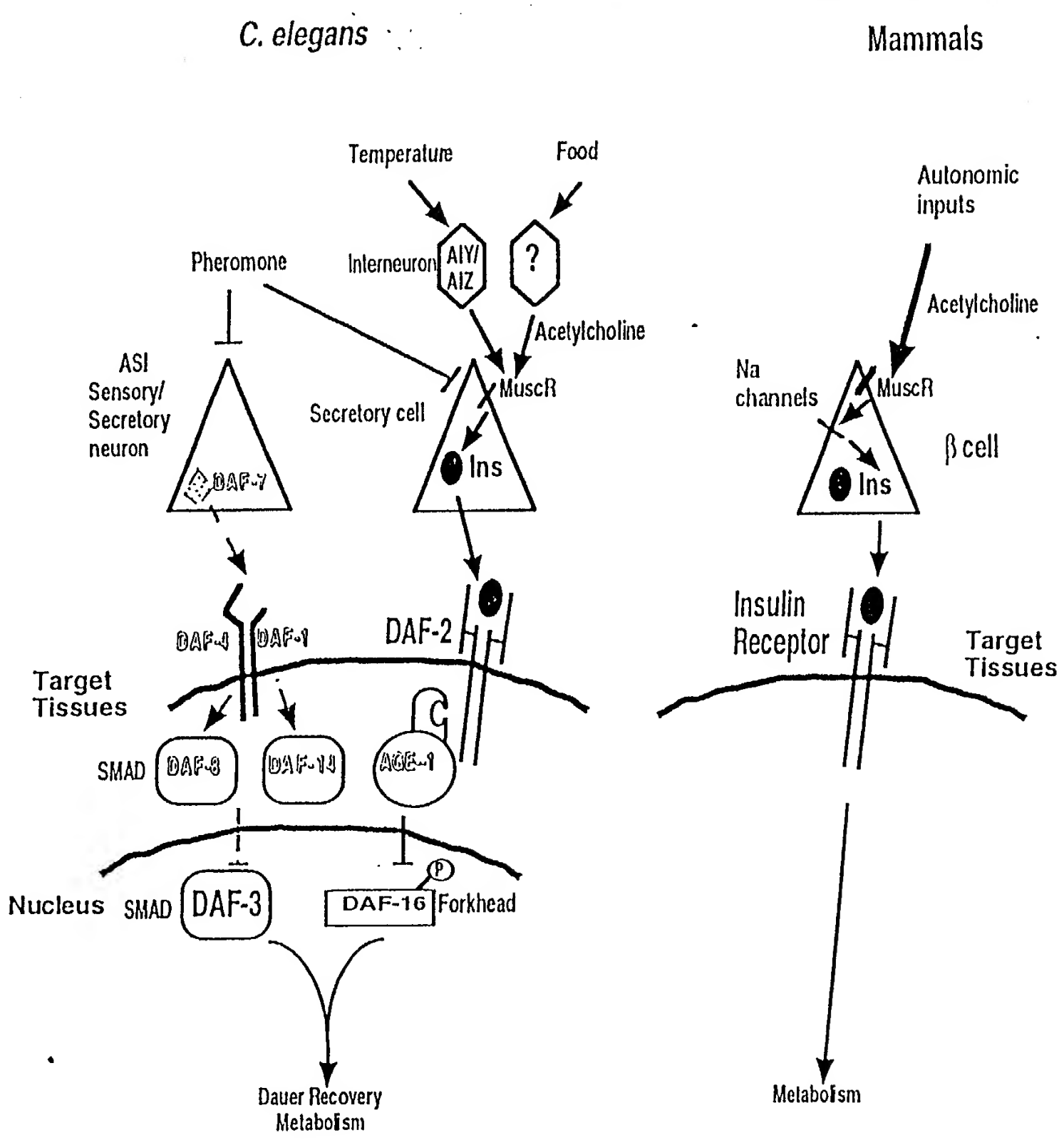

Dauer Recovery (%)
100
90
80
70
60
50
40
30
20
10
0
Temperature Downshift
Temperature Downshift/ Food
Temperature Downshift/ Food/ Atropine

FIG. 44C



with 1mM oxotremorine (C. elegans) or 0.5mM arecoline (A. caninum)


C. elegans
Mammals
Temperature
Food
Pheromone
Interneuron
AIY/
AIZ
?
Acetylcholine
ASI
Sensory/
Secretory
neuron
Secretory cell
MuscR
DAF-7
Ins
DAF-4
DAF-1
DAF-2
Target
Tissues
SMAD
DAF-8
DAF-14
AGE-1
Nucleus
SMAD
DAF-3
DAF-16
Forkhead
P
Dauer Recovery
Metabolism
Autonomic
inputs
Acetylcholine
Na
channels
MuscR
β cell
Ins
Insulin
Receptor
Target
Tissues
Metabolism

ATTCGGCATGAGCATGGaGCTTCGAGTCCTAGAGAACACAAAACGTTCCCGGCGGAACCTGGGtCTGGACTGCGAC
GAGACTCAAGCGAGTCCCGCTGCTGCCGATATCCCCTCACAGTGGACTTTGAGGCTTTCGGCTGGGACTGGATCAT
CGCACCTAAGCGCTACAAGGCCAACTACTGCTCCGGCCAGTGGGAGTACATGTTCATGCAAAAATATCCGCATACC
CATTTGGTGCAGCAGGCCAATCCAAGAGGTTATGcTGGGCCCTGTTGTACCCCCACCAAGATGTCCCCAATcAACA
TgcTctACTTCAATGACAAGCAGCAGATTATcTACGGCAAGATCCCTGGCATGGTGGTGGATCGCTGTGGcTGCTC
TTAAGGTGGGGGATAGAGGATGCCTCCCCCACAGACCGTACCCCAAGACCCATAGCCcTGCCCAATCCACCGCCTG
ATCCAAACAT

FIG. 47A

IRHEHGASSPREHKTFPAEPGSGLRRDSSESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGQWEYMFMQKYPHT
HLVQQANPRGYAGPCCTPTKMSPINMLYFNDKQQIIYGKIPLAMVVDRCGCS

FIG. 47B